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OM nucleic - nucleic search, using bw model

Run on: November 8, 2004, 20:41:41 / Search time 836 Seconds

(without alignments)
10304.187 Million cell updates/sec

Title: US-09-651-651-4

Perfect score: 1641
Sequence: 1 atgsgagcgcagcattcgaatc.....ctgataaagctgggacttaa 1641

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: N_Geneseq_23Sep04:*

1: geneseqn1980s:*\n2: geneseqn1990s:*\n3: geneseqn2000s:*\n4: geneseqn2001as:*\n5: geneseqn2001bs:*\n6: geneseqn2002as:*\n7: geneseqn2002bs:*\n8: geneseqn2003as:*\n9: geneseqn2003bs:*\n10: geneseqn2003cs:*\n11: geneseqn2003ds:*\n12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1641	100.0	1641	5 AAS01082	AAS01082 Arabidops
2	1622	98.8	1902	12 ADF47823	Adf47823 Arabidops
3	271.8	16.6	3896	3 AAC64438	AAC64438 Arabidops
4	271.8	16.6	3896	3 AAC64448	AAC64448 Arabidops
5	176.2	10.7	328	5 AAS01096	AAS01096 Corn ster
6	110.4	6.7	709	3 AAC64449	AAC64449 Lycopersi
7	110.4	6.7	709	3 AAC64439	AAC64439 Lycopersi
8	109	6.6	356	5 AAS01097	AAS01097 Corn ster
9	52.6	3.2	1872	12 ADF47831	Adf47831 Schizosac
10	49.4	3.0	1701	12 ADF47817	Adf47817 yeast mem
11	49.4	3.0	1986	3 AAC64431	AAC64431 Saccharom
12	49.4	3.0	1986	3 AAC64441	AAC64441 Saccharom
13	49.4	3.0	1986	3 AAC64440	AAC64440 Saccharom
14	49.4	3.0	1986	5 AAS01342	AAS01342 Yeast LCA
15	49.4	3.0	1986	12 ADF47816	Adf47816 Yeast acy
16	49.4	3.0	2000	8 ADA71938	Ada71938 Rice gene
17	47.4	2.9	2000	8 ADA71938	Ada71938 Rice gene
18	47.4	2.9	2312	3 AAC64442	AAC64442 Schizosac
19	47.4	2.9	2312	3 AAC64432	AAC64432 Schizosac
20	40.6	2.5	110000	2 AAV21209_12	Continuation (13 o
21	39.4	2.4	2223	12 ADF47830	Adf47830 Aspergill

C	22	38.8	2.4	486	4 AAF75507	AAf75507 Polygluta
	23	38.2	2.3	2047	12 ADF47829	Adf47829 Aspergill
	24	37.6	2.3	473	6 ABV94819	ABv94819 Human pan
	25	37.6	2.3	1292	10 ADC78228	Adc78228 Human sec
	26	37.6	2.3	3329	10 ADG32012	Adg32012 Human DNA
	27	37.6	2.3	3356	12 ADH22401	Adh22401 Human CDN
	28	37.6	2.3	3737	6 AAS94885	AAS94885 Human DNA
	29	37.6	2.3	11477	4 ABL17946	ABl17946 Drosophi
	30	37.6	2.3	12600	4 ABL17948	ABl17948 Drosophi
	31	37.6	2.3	12600	4 ABL17952	ABl17952 Drosophi
	32	37.6	2.3	12600	4 ABL27368	ABl27368 Drosophi
	33	36.4	2.2	296	5 ABV18850	ABv18850 Human pro
	34	36.4	2.2	110000	6 ABA90521_16	Continuation (17 o
	35	36	2.2	2433	9 AAL62907	AAI62907 Rice CDNA
	36	36	2.2	3579	3 AAL70099	AAI70099 Plasmodi
	37	35.8	2.2	2016	12 ADF47833	Adf47833 Creple pa
	38	35.8	2.2	2976	4 ABA03653	ABa03653 Murine A
	39	35.8	2.2	4590	5 AAH24065	AaH24065 Yeast AOD
	40	35.8	2.2	266145	10 ADEB7477	AdEB7477 Fowlpox v
	41	35.6	2.2	2356	6 AAS62537	AAS62537 CDNA sequ
	42	35.6	2.2	4089	4 AAL37519	AAI37519 Human mus
	43	35.6	2.2	4089	8 ABX60507	ABx60507 CDNA enco
	44	35.6	2.2	4089	12 ADJ31257	Adj31257 Human mus
	45	35.6	2.2	17703	6 ABK39953	ABk39953 Human che

ALIGNMENTS

RESULT 1	AAS01082	standard; DNA; 1641 BP.
ID	AAS01082	
XX	AC	AAS01082;
XX	AC	
DT	31-MAY-2001	(first entry)
XX	XX	
DE	Arabidopsis thaliana sterol acyltransferase LCAT2 DNA.	
XX	XX	
KW	Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;	
KW	acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;	
KW	nutritional supplement; dairy product; food product; salad dressing; ds.	
XX	XX	
OS	Arabidopsis thaliana.	
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	1..1641
FT	FT	/*tag= a
FT	FT	/product= "LCAT2"
XX	XX	
PN	W0200116308-A2.	
XX	XX	
PD	08-MAR-2001.	
XX	XX	
PF	30-AUG-2000; 2000WO-US023863.	
XX	XX	
PR	30-AUG-1999; 99US-0152493P.	
XX	XX	
PA	(MONS) MONSANTO CO.	
PI	Laesner M, Van Eenennaam A;	
XX	XX	
DR	WPI: 2001-169010/17.	
DR	P-PSDB; AAU00459.	
XX	XX	
PT	New isolated nucleic acid encoding plant lecithin:cholesterol	
PT	acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase	
PT	-like polypeptides, for modifying the sterol content and oil production	
PT	of plants.	
XX	XX	
PS	Claim 5; Page 77; 127pp; English.	
XX	XX	
CC	The present sequence encodes for Arabidopsis thaliana	

lecithin:cholesterol acyltransferase-like 2 (LCAT2). Several novel
polynucleotides encoding the plant sterol acyltransferases LCAT
(AA5001081-AA501104, AA501341) and ACAT (acyl CoA:cholesterol
acyltransferase-like; AA501311-AA501319) are described. A yeast LCAT
related open reading frame, LRO1 gene sequence (AA501342), and a rat ACAT
(AA501105) cDNA sequence are also described. The polynucleotides encoding
LCAT or ACAT are used to produce LCAT or ACAT polypeptides. They can also
be used in a recombinant construct to transform a host cell (preferably
of a plant) or a plant. The recombinant construct is used to increase or
decrease the sterol content of the host cell or plant. It can be used to
alter oil production of the plant or plant, preferably by increasing it.
The oil of the plant or the plant itself is used as a food product, or as
nutritional or dietary supplements, or in pharmaceutical compositions for
lowering cholesterol. The oil can be used in foods e.g. margarine,
butter, cooking oil, and dressings e.g. salad dressings, mayonnaise,
cheese, processed meat, pasta, sauces, cereals, desserts, dips, chips,
baked goods, pastries, cookies, snack bars, confections, chocolates, and
beverages. The alteration in sterol content and/or composition can also
provide a plant with tolerance to stress and insect damage

Sequence 1641 BP; 438 A; 355 C; 378 G; 470 T; 0 U; 0 Other;

Query Match 100.0%; Score 1641; DB 5; Length 1641;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGGCAATTCGAAATCAGTAACGCGCTTCCTTCAACCGTCATCGCCGTTTTTCTTG 60

DB 1 ATGGAGGCAATTCGAAATCAGTAACGCGCTTCCTTCAACCGTCATCGCCGTTTTTCTTG 60

QY 61 ATTTGGCGGTGGCCGAACCTGCGGTGAGAGATGAGACCGAGTTTCACGGGACTACTCGAAG 120

DB 61 ATTTGGCGGTGGCCGAACCTGCGGTGAGAGATGAGACCGAGTTTCACGGGACTACTCGAAG 120

QY 121 CTATCGGGGTATATATCATTCGCGGATTTTGGTCAAGCAGCAGCTACGAGCGTGGCGATCTT 180

DB 121 CTATCGGGGTATATATCATTCGCGGATTTTGGTCAAGCAGCAGCTACGAGCGTGGCGATCTT 180

QY 181 GACTGTCCATACACTCCGTTGAGCTTCAATCCGCTCGACTGTATGCTAGACACCACT 240

DB 181 GACTGTCCATACACTCCGTTGAGCTTCAATCCGCTCGACTGTATGCTAGACACCACT 240

QY 241 AAGCTTCTTTCTGCTGTCACTGCTGTTTAAGTATAGTGTCTAGATCTTATATATAA 300

DB 241 AAGCTTCTTTCTGCTGTCACTGCTGTTTAAGTATAGTGTCTAGATCTTATATATAA 300

QY 301 ACAGACCATCCCGAGGTGAAGTCAAGGCTGACAGTGTCTTTCAGCCATACAGAAATG 360

DB 301 ACAGACCATCCCGAGGTGAAGTCAAGGCTGACAGTGTCTTTCAGCCATACAGAAATG 360

QY 361 GATCCAGGTTACATTAACAGTCTCTTTCTACTGTCTGAAAGAGTGGCTTAAGTGTGT 420

DB 361 GATCCAGGTTACATTAACAGTCTCTTTCTACTGTCTGAAAGAGTGGCTTAAGTGTGT 420

QY 421 GTTGAATTTGGTATGAAGCAATGCAATTTGCTGTTCCATACGATTTGAGATTTGCA 480

DB 421 GTTGAATTTGGTATGAAGCAATGCAATTTGCTGTTCCATACGATTTGAGATTTGCA 480

QY 481 CCAACCAATTTGGAAGAGAGCTTACTTCACTTCAAGCTCAAGTTGACCTTTGAAACT 540

DB 481 CCAACCAATTTGGAAGAGAGCTTACTTCACTTCAAGCTCAAGTTGACCTTTGAAACT 540

QY 541 GCTTTAAATCTCCGTGGCGGCCCTTCTATAGTATTTGGCCATTCAATGGATATATATGTC 600

DB 541 GCTTTAAATCTCCGTGGCGGCCCTTCTATAGTATTTGGCCATTCAATGGATATATATGTC 600

QY 601 TTGAGATCTTTCTGGAATGGCTGAGGCTAAGAAATGCAACAAACATTAATTTGAAGTGG 660

DB 601 TTGAGATCTTTCTGGAATGGCTGAGGCTAAGAAATGCAACAAACATTAATTTGAAGTGG 660

QY 661 CTTGATCGCATATCATGCTTAATTCGCTGTGAGAGCTCTCTTCTTGTTCTGTTGAG 720

DB 661 CTTGATCGCATATCATGCTTAATTCGCTGTGAGAGCTCTCTTCTTGTTCTGTTGAG 720

QY 721 GCAATCAATCTACTCTCTGTGTGAACGTTTGACCTTCTCTGTTTCTGAGGAACTGCT 780

DB 721 GCAATCAATCTACTCTCTGTGTGAACGTTTGACCTTCTCTGTTTCTGAGGAACTGCT 780

QY 781 CGGTTGTTGCCAATCTCTTTTGGTGGTCAATGTGGGCTTATGCCATTTTCAAGAAATGCG 840

DB 781 CGGTTGTTGCCAATCTCTTTTGGTGGTCAATGTGGGCTTATGCCAATTTTCAAGAAATGCG 840

QY 841 AAGGATATTAACATCTCGGACGCAATTTTCTGCGGGGTGCTGCAAGAAAGATTAAGCGC 900

DB 841 AAGGATATTAACATCTCGGACGCAATTTTCTGCGGGGTGCTGCAAGAAAGATTAAGCGC 900

QY 901 GTATACCACTGTGTGAAGAGAAATATCAATCAAAATATTTCTGCTGGCCCAAAATATT 960

DB 901 GTATACCACTGTGTGAAGAGAAATATCAATCAAAATATTTCTGCTGGCCCAAAATATT 960

QY 961 ATTAACTTGAATTCCTTCCACAGGCTTACAGAAACAGCTCATGCAATGACAGCAGC 1020

DB 961 ATTAACTTGAATTCCTTCCACAGGCTTACAGAAACAGCTCATGCAATGACAGCAGC 1020

QY 1021 ATGGAATGTGGCTTCCACCCCTTTTGTCTTTCACAGCCCGTGAACCTAGCAGATGGAGCT 1080

DB 1021 ATGGAATGTGGCTTCCACCCCTTTTGTCTTTCACAGCCCGTGAACCTAGCAGATGGAGCT 1080

QY 1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGATGTTACACCAATTAAAG 1140

DB 1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGATGTTACACCAATTAAAG 1140

QY 1141 AAGTTGATATATATGATGACCCGTTTATATCTGTGCTCTTGGGAGAGACCACTATA 1200

DB 1141 AAGTTGATATATATGATGACCCGTTTATATCTGTGCTCTTGGGAGAGACCACTATA 1200

QY 1201 AAAAATGATTTTGCATATATAGTGTCTCATCTAAAGACAGAGTGTGTTATTACTTGGCC 1260

DB 1201 AAAAATGATTTTGCATATATAGTGTCTCATCTAAAGACAGAGTGTGTTATTACTTGGCC 1260

QY 1261 CCAAGTGGCAAACTTATCTGATATATGATGATCATCAAGATATCATTTACGAAACTGAA 1320

DB 1261 CCAAGTGGCAAACTTATCTGATATATGATGATCATCAAGATATCATTTACGAAACTGAA 1320

QY 1321 GGTTCCTCGTGTCAAGGTCTGGAACGTGTGTGATGAGAAAGCTGGAACCTATACTGGG 1380

DB 1321 GGTTCCTCGTGTCAAGGTCTGGAACGTGTGTGATGAGAAAGCTGGAACCTATACTGGG 1380

QY 1381 GATGAGACGATACCTATCATCTCTCTTGTGCAAGAAATTTGGCTCGGACTTAAGTT 1440

DB 1381 GATGAGACGATACCTATCATCTCTCTTGTGCAAGAAATTTGGCTCGGACTTAAGTT 1440

QY 1441 AACATTAACATGCTCCCAAGCAGAAACAGATGGAAGCGATCATGTGGAACCTAAAT 1500

DB 1441 AACATTAACATGCTCCCAAGCAGAAACAGATGGAAGCGATCATGTGGAACCTAAAT 1500

QY 1501 GTTATGATAGCATGTGGGTGAGACATATAGCTTAACATGACAAAGACCAAGGGTTAAG 1560

DB 1501 GTTATGATAGCATGTGGGTGAGACATATAGCTTAACATGACAAAGACCAAGGGTTAAG 1560

QY 1561 TACATTAACCTTTTATGAAGACTCTGAGAGCAATTCGGGGGAGAGAACCGGAGCTGGAG 1620

DB 1561 TACATTAACCTTTTATGAAGACTCTGAGAGCAATTCGGGGGAGAGAACCGGAGCTGGAG 1620

QY 1621 CTTGATTAAGTGGGTTATTA 1641

DB 1621 CTTGATTAAGTGGGTTATTA 1641

RESULT 2

ADP47823

ID ADP47823 standard; DNA; 1902 BP.

XX ADP47823;

AC

XX 26-FEB-2004 (first entry)

Arabidopsis thaliana acyltransferase nucleotide sequence SEQ ID NO:8.

acyltransferase; enzyme; membrane-spanning region;
active membrane independent acyltransferase; fatty acid ester;
fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol;
phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;
acylated amino acid; structured lipid; fat-soluble molecule; gene; ds.

Arabidopsis thaliana.

MO2003100044-A1.

04-DEC-2003.

28-MAY-2003; 2003WO-SE000870.

29-MAY-2002; 2002SE-00001581.
29-MAY-2002; 2002US-0383889P.
20-JAN-2003; 2003SE-00000142.

(SCAN1) SCANDINAVIAN BIOTECHNOLOGY RES AB.

Dahlqvist A, Ghosal A, Lindqvist Y, Banas A;
WPI; 2004-053268/05.
P-PSDB; ADF47824.

New nucleotide sequence encoding an improved acyltransferase polypeptide,
useful for producing structured lipids or fat-soluble molecules, in
removing undesirable fat or in modifying lipids in animal or plant raw
material.

Claim 5; SEQ ID NO 8; 91pp; English.

The present invention describes a nucleotide sequence (I) derived from a
nucleotide sequence encoding an acyltransferase polypeptide comprising at
least one membrane-spanning region. (I) encodes an improved active
membrane independent acyltransferase polypeptide in which at least one
amino acid residue of the membrane-spanning region has been deleted
and/or substituted as compared to the original acyltransferase
polypeptide, where the encoded active membrane independent
acyltransferase polypeptide can produce fatty acid esters and/or fatty
acid thioesters such as triacylglycerols, diacylglycerols,
monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters,
acylated carbohydrates and acylated amino acids. Also described: (1) a
nucleotide sequence molecule (II) comprising at least one promoter region
which functions in a host, where the promoter region is operably linked
to at least one (I), which is operably linked to at least one non-
translated region which functions in a host; (2) a vector comprising (II)
(3) a host cell comprising (II) or the vector; (4) producing an
improved active membrane independent acyltransferase polypeptide,
comprising providing the above host cell and a growth medium preparing a
host cell culture, culturing the host cell culture and harvesting the
host cell culture and recovering the improved active membrane independent
acyltransferase polypeptide; (5) a polypeptide obtained by the method in
(4), where the polypeptide at least is an improved active membrane
independent acyltransferase polypeptide; (6) an oligonucleotide
specifically hybridizing to (I) under stringent conditions; and (7) a kit
comprising the above polypeptide and a stabilizer. The nucleic acid
molecule (I) and the polypeptide are useful in producing structured
lipids or fat-soluble molecules, in removing undesirable fat or in
modifying lipids present in animal and plant raw material. The present
sequence is used in the exemplification of the present invention.

Sequence 1902 BP, 516 A; 405 C; 444 G; 537 T; 0 U; 0 Other;

Query Match 98.8%; Score 1622; DB 12; Length 1902;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 5; Indels 0; Gaps 0.

1 ATGGAGCGAATTCGAATCAGTAACGGCTTCCTACCGTCATCGCGGTTTTTTCTTG 60

Db	1	ATGGAGGAAATTGGAAATCAGTAACGAGCTTCCTTACCGCTCATCGCCGTTTCTTTCCTTG	60
Qy		ATTGGCGGTGGCCGGAATCTGCGGTGAGAGATTAAGACCCGATTTCAACGGCGACTACTCCGAG	120
Db	61	ATTGGCGGTGGCCGGAACGGCGGTGAGAGATTAAGACCCGATTTCAACGGCGACTACTCCGAG	120
Qy		CTATCGGGGTATTAATCAATTCGCGGAAATTGGCGGTGAGAGATTAAGACCCGATTTCAACGGCG	180
Db	121	CTATCGGGGTATTAATCAATTCGCGGAAATTGGCGGTGAGAGATTAAGACCCGATTTCAACGGCG	180
Qy		GACTGTCCATACACTCCGTTGGAATTCGATCGGCTGCACTCGATATGAGCTATGACACCACT	240
Db	181	GACTGTCCATACACTCCGTTGGAATTCGATCGGCTGCACTCGATATGAGCTATGACACCACT	240
Qy	241	AAGCTTCTTCTGCTGTCACTGCTGGTTTAAGTGTATGCTGATGATCTTTATATCA	300
Db	241	AAGCTTCTTCTGCTGTCACTGCTGGTTTAAGTGTATGCTGATGATCTTTATATCA	300
Qy	301	AACAGCAATCCCGAGTGTAACTCAACGCGCTGACAGTGGTCTTACGCAATCAGAAATG	360
Db	301	AACAGCAATCCCGAGTGTAACTCAACGCGCTGACAGTGGTCTTACGCAATCAGAAATG	360
Qy	361	GATCCAGGTATCAATACAGTCTCTTCTTCTACTGTCTGAAAGAGTGGCTTAACTGATG	420
Db	361	GATCCAGGTATCAATACAGTCTCTTCTTCTACTGTCTGAAAGAGTGGCTTAACTGATG	420
Qy	421	GTTGAGTTGGTATAGAAAGCAATATGCAATGTCGCTGTTCCATACGATGAGATTTGCA	480
Db	421	GTTGAGTTGGTATAGAAAGCAATATGCAATGTCGCTGTTCCATACGATGAGATTTGCA	480
Qy	481	CCAACCAATTTGGAAGAGCGTGACCTTTACTTTACAAAGCTCAAGTTGACCTTTGAACT	540
Db	481	CCAACCAATTTGGAAGAGCGTGACCTTTACTTTACAAAGCTCAAGTTGACCTTTGAACT	540
Qy	541	GCTTAAACCTCCGCGGCGCCCTTCTTAATGATATTTGGCCATTCAATGGGTAATATATGC	600
Db	541	GCTTAAACCTCCGCGGCGCCCTTCTTAATGATATTTGGCCATTCAATGGGTAATATATGC	600
Qy	601	TTGAGATCTTTCGAAATGGCTAGAGGTAGAAATGCAACCAAAACATTATTTGAAGTGG	660
Db	601	TTGAGATCTTTCGAAATGGCTAGAGGTAGAAATGCAACCAAAACATTATTTGAAGTGG	660
Qy	661	CTTGATCAGCATATCCATGCTTATTTGGCTGTGGAAGTCTCTCTTCTTGGTTCTGTGAG	720
Db	661	CTTGATCAGCATATCCATGCTTATTTGGCTGTGGAAGTCTCTCTTCTTGGTTCTGTGAG	720
Qy	721	GCAATCAAAATCTACTCTCTGCTGTGTAACGTTGGCCCTCTCTGTTTTCGAGGAACTGCT	780
Db	721	GCAATCAAAATCTACTCTCTGCTGTGTAACGTTGGCCCTCTCTGTTTTCGAGGAACTGCT	780
Qy	781	CGGTGTGTGCCAATTCCTTTTGGCGTGTCAATGTGTGCTTATGCCATTTTCAAGAAATTGC	840
Db	781	CGGTGTGTGTGCCAATTCCTTTTGGCGTGTCAATGTGTGCTTATGCCATTTTCAAGAAATTGC	840
Qy	841	AAGGTTGTAACAATCTCTGAGCGCATTTTCTGCGGGTGTCTGCAAGAAAGATTAAGCGC	900
Db	841	AAGGTTGTAACAATCTCTGAGCGCATTTTCTGCGGGTGTCTGCAAGAAAGATTAAGCGC	900
Qy	901	GTATATCCATCTGTGTAAGAGGAATATCAATCAAAATATTTGGCTGGCGCAAAATATTT	960
Db	901	GTATATCCATCTGTGTAAGAGGAATATCAATCAAAATATTTGGCTGGCGCAAAATATTT	960
Qy	961	ATTAAATTTGAAATTCCTTCCATAGCGTTTACAGAAACAGCTCTTATGTCATGATCAGC	1020
Db	961	ATTAAATTTGAAATTCCTTCCATAGCGTTTACAGAAACAGCTCTTATGTCATGATCAGC	1020
Qy	1021	ATGGAATGTGGCTTCCACCCCTTTTGTCTTTCACAGCCGCTGAATAGCAGATGGGACT	1080
Db	1021	ATGGAATGTGGCTTCCACCCCTTTTGTCTTTCACAGCCGCTGAATAGCAGATGGGACT	1080
Qy	1081	CTTTTCAAGCAATAGAAATATAGACCCGAGATGCAAGAGAGATTTACACAGTTAAAG	1140
Db	1081	CTTTTCAAGCAATAGAAATATAGACCCGAGATGCAAGAGAGATTTACACAGTTAAAG	1140

```
Qy 1141 AAGTTGATCATGATGACCTGTTTAACTCTGACTCCTTGGAGAGCACTATA 1200
    |||
Db 1141 AAGTTGATCATGATGACCTGTTTAACTCTGACTCCTTGGAGAGCACTATA 1200
Qy 1201 AAAAATGATTTTGGATATATGAGCTCATTAAGAGAGGTTGGTTATTAAGTGGC 1260
    |||
Db 1201 AAAAATGATTTTGGATATATGAGCTCATTAAGAGAGGTTGGTTATTAAGTGGC 1260
Qy 1261 CCAAGTGGCAAACTTATCTGATTAATTGATCATCAGATATCATTTTACGAACTGAA 1320
    |||
Db 1261 CCAAGTGGCAAACTTATCTGATTAATTGATCATCAGATATCATTTTACGAACTGAA 1320
Qy 1321 GGTTCCTCTGTTGCAAGGTTGGAACCTGTGTTGATGGGAAAGCTGGAAGCTTAACTGGG 1380
    |||
Db 1321 GGTTCCTCTGTTGCAAGGTTGGAACCTGTGTTGATGGGAAAGCTGGAAGCTTAACTGGG 1380
Qy 1381 GATGAGACGGTACCTTATCATCTCTCTGTTGCAAGAAATTTGGCTGGACCTTAAAGTT 1440
    |||
Db 1381 GATGAGACGGTACCTTATCATCTCTCTGTTGCAAGAAATTTGGCTGGACCTTAAAGTT 1440
Qy 1441 AACATTAACATGAGTCCCGACGACAGACAGATGGAACGACATATGGAATTAAT 1500
    |||
Db 1441 AACATTAACATGAGTCCCGACGACAGACAGATGGAACGACATATGGAATTAAT 1500
Qy 1501 GTTGATCATGAGCATGGGTGACATCATAGCTTAACATGACAAAGCAAGGTTAAG 1560
    |||
Db 1501 GTTGATCATGAGCATGGGTGACATCATAGCTTAACATGACAAAGCAAGGTTAAG 1560
Qy 1561 TACATTAACCTTTTGAAGACTCTGAGAGCAATTCGGGGAAAGAAAGCGAGTGGGAG 1620
    |||
Db 1561 TACATTAACCTTTTGAAGACTCTGAGAGCAATTCGGGGAAAGAAAGCGAGTGGGAG 1620
Qy 1621 CTTGATTAATA 1630
    |||
Db 1621 CTTGATTAATA 1630

RESULT 3
AAC64438
ID AAC64438 standard; DNA; 3896 BP.
XX
AC AAC64438;
XX
DT 12-FEB-2001 (first entry)
DE Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:11.
XX
KW PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KM EST; expressed sequence tag; fatty acid; oil content; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200060095-A2.
XX
PD 12-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-EP002701.
XX
PR 01-APR-1999; 99EP-00106656.
PR 10-JUN-1989; 99EP-00111321.
PR 07-FEB-2000; 2000US-0180687P.
XX
PA (BAD1 ) BASF PLANT SCI GMBH.
XX
PI Dahlqvist A, Stahl U, Lenman M, Banas A, Romme H, Szymme S;
DR WPI; 2000-665012/64.
XX
PT Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT pathway for triacylglycerol production and DNAs encoding them, useful for
PT producing triacylglycerol, or for transforming any cell or organism to
PT increase oil content.
```

```
XX
PS Claim 6; Page 60-61; 97pp; English.
XX
CC The present invention describes an enzyme for catalysing (in an acyl-CoA-
CC independent reaction) the transfer of fatty acids from phospholipids to
CC diacylglycerol in the biosynthetic pathway for the production of
CC triacylglycerol (TAG). The enzyme is designated as
CC phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
CC nucleotides encoding them are useful for producing TAG and/or TAG with
CC uncommon fatty acids. The enzyme and the nucleotide are also useful for
CC transforming any cell or organism in order to be expressed in this cell
CC or organism and result in an altered, preferably increased oil content of
CC this cell or organism. The present sequence represents the Arabidopsis
CC thaliana PDAT genomic DNA
XX
SQ Sequence 3896 BP; 1042 A; 725 C; 769 G; 1360 T; 0 U; 0 Other;
XX
Query Match 16.6%; Score 271.8; DB 3; Length 3896;
Best Local Similarity 80.0%; Pred. No. 1,66-74;
Matches 375; Conservative 0; Mismatches 2; Indels 92; Gaps 1;
Qy 768 TGAAGGAACCTGCTGGTGTGTTGTCATTTCTTTGCTGTCATTTGCTTATGCAATT 827
    |||
Db 1787 TCAAGGAACCTGCTGGTGTGTTGTCATTTCTTTGCTGTCATTTGCTTATGCAATT 1846
Qy 828 TTCAAAGAAATTTGCAAGGCTGATTAACATCTGGAAGCATTTTCTGGGGTGTGCAAA 887
    |||
Db 1847 TTCAAAGAAATTTGCAAGGCTGATTAACATCTGGAAGCATTTTCTGGGGTGTGCAAA 1906
Qy 888 GAAAGATTAAGGCGGTATTAACCACTGTGATGAAGAGATATCAATAATTTCTGGCTG 947
    |||
Db 1907 GAAAGATTAAGGCGGTATTAACCACTGTGATGAAGAGATATCAATAATTTCTGGCTG 1966
Qy 948 GCCGACAATATTTTAACTTGAATTCCTTCAGTAGC----- 987
    |||
Db 1967 GCCGACAATATTTTAACTTGAATTCCTTCAGTAGC----- 2026
Qy 988 ----- 987
    |||
Db 2027 ACTGTAACTTAACMAAAGTTTCAACAAGATGTTCACTGATATTTGTTCTTTGAT 2086
Qy 988 -----GTTACGAAACAGCTCTAGTCAACATGACACCATGAAATGAGCCTT 1035
    |||
Db 2087 GTGTATCCATCAGTTTACGAAACAGCTCTAGTCAACATGACACCATGAAATGAGCCTT 2146
Qy 1036 CCCACCTTTTGTCTTTCACAGCCCGTGAACCTAGACAGATGGGACTTTTCAAGCAATA 1095
    |||
Db 2147 CCCACCTTTTGTCTTTCACAGCCCGTGAACCTAGACAGATGGGACTTTTCAAGCAATA 2206
Qy 1096 GAAGACTATGACCCAGATAGCAAGAGATGTTTACACAGTTTAAAGAGT 1144
    |||
Db 2207 GAAGACTATGACCCAGATAGCAAGAGATGTTTACACAGTTTAAAGAGT 2255

RESULT 4
AAC64448
ID AAC64448 standard; DNA; 3896 BP.
XX
AC AAC64448;
XX
DT 12-FEB-2001 (first entry)
DE Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:10b.
XX
KW PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KM EST; expressed sequence tag; fatty acid; oil content; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200060095-A2.
XX
PD 12-OCT-2000.
```


Db 154 CTGAGACCCGGTTATTATACAGGTCCCTCTCTCTTCAAGTATGAGAAAGAAATGGCTCAATGG 213

Qy 418 TGTGTGAGTTTGGTGTATAGAGCAAAATGCATTTGTGGCTTGTCCATTACGATTTGGAGATTG 477

Db 214 TGTGTAGAGTTTGGCATTAAGCTAATGCAATTATGCTGTGTCGATTGATTTGAGACTG 273

Qy 478 TCACCAACCAAAATGGAGAGCGCTGACCTTTACTTTACAA 518

Db 274 CCCCATCAATGCTTGTAGAGAGAGATCTGTATCTTTACAA 314

RESULT 6

ID	AAC64449	Standard;	CDNA;	709	BP.

DT 12-FEB-2001 (first entry)

DE Lycopersicon esculentum PDAT nucleotide sequence SEQ ID NO:11b.

KM PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG
KM EST; expressed sequence tag; fatty acid; oil content; ss.

05 *Lycopersicon esculentum*.

PN WO200060095-A2.

PD 12-OCT-2000.

PF 28-MAR-2000; 2000WO-EP002701.

PR 01-APR-1999; 99EP-00106656.

PR 07-FEB-2000; 2000US-0180687P.PA (BADI) BASF PLANT SCI GMBH.

PI Dahlqvist A, Stahl U, Lenman M, Banas A, Ronne H, Styrmne S;

DR WPI; 2000-665012/64.

Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic pathway for triacylglycerol production and DNAs encoding them, useful for producing triacylglycerol, or for transforming any cell or organism to increase oil content.

PS Claim 6; Page 97; 97pp; English.

CC The present invention describes an enzyme for catalysing (in an acyl-CoA-
CC independent reaction) the transfer of fatty acids from phospholipids to
CC diacylglycerol in the biosynthetic pathway for the production of
CC triacylglycerol (TAG). The enzyme is designated as
CC phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
CC nucleotides encoding them are useful for producing TAG and/or TAG with
CC uncommon fatty acids. The enzyme and the nucleotide are also useful for
CC transforming any cell or organism in order to be expressed in this cell
CC or organism and result in an altered, preferably increased oil content of
CC this cell or organism. The present sequence represents the Lycopodium
CC esculentum PDAT nucleotide sequence

SQ Sequence 709 BP; 226 A; 121 C; 161 G; 201 T; 0 U; 0 Other;

Query Match	6.7%	Score 110.4;	DB 3	Length 709;
Best Local Similarity	74.5%	Pred. No. 9.5e-24;		
Matches 152; Conservative	0;	Mismatches -51;		Indels 1;
				Gaps 1;

Qy 1426 CTCGGACCTTAAAGTTTAAACATTAACAATGGCTTCCCGACGCCAATAACAGTAGGAGCGACGTA 1495

Dp 1 CTGGGGCCCAAAAGTGAATTAACAAGGACACCCAGTCAAGCAGCAT -GTTTCAGATGTA 59

1486 CATGTGGAACCTAAATGTTGATCATGAGCATGGTGCAGACATCATAGCTAACATGCAAAA 1545

Db	6	CNAAGTCATCTAAATTATGAGCATCAACATGCTGAAGTATCATCTCCCAATTATGCAAAAG	119
Qy	1546	GCACCCAAAGGGTTAAGTACATACCTTTTATGAAAGCTTGGAGAGCATTTCCGGGGAAGA	1605
Db	120	TTACTCTCAATGAAGTACATATACTATTATGAGATTCTGAAAGTTTCCAGGCAAGA	179
Qy	1606	ACCGCAGTCTGGAGCTTGATMAA	1629
Db	180	ACAGCAGTTTGGAGCTTGATMAA	203

RESULT 7

ID AAC64439 standard; cDNA; 709 BP.

AC AAC64439;

DT 12-FEB-2001 (first entry)

DE	Lycopersicon esculentum	PDAT nucleotide sequence	SEQ ID NO:12.
DE			

KM PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KM EST; expressed sequence tag; fatty acid; oil content; ss.

05 Lycopersicon esculentum.

PN WO200060095-A2.

PD 12-OCT-2000.

PF 28-MAR-2000; 2000WO-EP002701.

PR 01-APR-1999; 99EP-00106656.

PR 07-FEB-2000; 2000US-0180687P.PA (BADI) BASF PLANT SCI GMBH.

PI Dahlqvist A, Stahl U, Lenman M, Baras A, Ronne H, Styrmne S;

DR WPI; 2000-665012/64.

Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic pathway for triacylglycerol production and DNAs encoding them, useful for producing triacylglycerol, or for transforming any cell or organism to increase oil content.

PS Claim 6; Page 62; 97pp; English.

The present invention describes an enzyme for catalysing (in an acyl-CoA-independent reaction) the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol (TAG). The enzyme is designated as phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the nucleotides encoding them are useful for producing TAG and/or TAG with uncommon fatty acids. The enzyme and the nucleotide are also useful for transforming any cell or organism in order to be expressed in this cell or organism and result in an altered, preferably increased oil content of this cell or organism. The present sequence represents the Lycopodium esculentum PDAT nucleotide sequence

Sequence 709 BP; 226 A; 120 C; 162 G; 201 T; 0 U; 0 Other;

Query Match	6.7%	Score 110.4;	DB 3;	Length 709;
Best Local Similarly	74.5%	Pred. No. 9.5e-24;		
Matches 152; Conservative	0;	Mismatches 51;	Indels 1;	Gaps 1;

Qy 1426 CTCGGACCTTAAGTTAACTAATACATGCGTCTCCCGAGCCAGAACGATGAGAGCGACGTA 1485

QY 1486 CATCTGAACTAATGTTGATCATGAGCATGGTCAGACATCATAGCTAACATGCAGAAA 1545

DB 60 CAAGTCATCTTAAATATAGACATCAACATGATGAGATATATCCCAATATAGCAAAAG 119
 QY 1546 GCACCAAGGTTAAGTACATTAACCTTTATGAAAGCTCTGAGAGACATTCGGGGAAGAGA 1605
 DB 120 TTACCTACATGAAAGTACATTAACCTATTTATGAGATCTGAAAGTTTCCAGGACAAAGA 179
 QY 1606 ACCGAGCTCTGGAGCTTGATPAA 1629
 DB 180 ACAGCAGTTTGGAGACTTGATPAA 203

RESULT 8

AAS01097
 ID AAS01097 standard; cDNA; 356 BP.

AC AAS01097;

DT 31-MAY-2001 (first entry)

DE Corn sterol acyltransferase LCAT EST sequence #4.

KW Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;
 KM acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;
 KM nutritional supplement; dairy product; food product; salad dressing;
 KM corn; Arabidopsis thaliana; expressed sequence tag; EST; ss.

XX Zea mays.

OS WO200116308-A2.

PN 08-MAR-2001.

PD 30-AUG-2000; 2000WO-US023863.

XX 30-AUG-1999; 98US-0152493P.

PR (MONS) MONSANTO CO.

PA Laesener M, Van Benneham A;

PI WPI; 2001-169010/17.

XX New isolated nucleic acid encoding plant lecithin:cholesterol
 PT acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase
 PT -like polypeptides, for modifying the sterol content and oil production
 PT of plants.

PS Claim 5; Page 90; 127pp; English.

XX The present sequence for corn LCAT (lecithin:cholesterol acyltransferase-
 CC like) EST sequence #4 is closely related to the Arabidopsis thaliana
 CC LCAT2 sequence. Several novel polynucleotides encoding the plant sterol
 CC acyltransferases LCAT (AAS001081-AAS01104, AAS01341) and ACAT (acyl
 CC CoA:cholesterol acyltransferase-like; AAS0111-AAS01319) are described. A
 CC yeast LCAT related open reading frame, LRO1 gene sequence (AAS01342), and
 CC a rat ACAT (AAS01105) cDNA sequence are also described. The
 CC polynucleotides encoding LCAT or ACAT are used to produce LCAT or ACAT
 CC polypeptides. They can also be used in a recombinant construct to
 CC transform a host cell (preferably of a plant) or a plant. The recombinant
 CC construct is used to increase or decrease the sterol content of the host
 CC cell or plant. It can be used to alter oil production of the cell or
 CC plant, preferably by increasing it. The oil of the plant or the plant
 CC itself is used as a food product, or as nutritional or dietary
 CC supplements, or in pharmaceutical compositions for lowering cholesterol.
 CC The oil can be used in foods e.g. margarine, butter, cooking oil, and
 CC dressings e.g. salad dressings, mayonnaise, cheese, processed meat,
 CC pasta, sauces, cereals, desserts, dips, chips, baked goods, pastries,
 CC cookies, snack bars, confections, chocolates, and beverages. The
 CC alteration in sterol content and/or composition can also provide a plant
 CC with tolerance to stress and insect damage

XX Sequence 356 BP; 98 A; 80 C; 78 G; 100 T; 0 U; 0 Other;

Query Match 6.6%; Score 109; DB 5; Length 356;
 Best Local Similarity 76.1%; Pred. No. 1.8e-23;
 Matches 150; Conservative 0; Mismatches 40; Indels 7; Gaps 1;

QY 338 GTCTTACGATCAGCAAAATTTGATCCAGCTTCAATPAA-----CAGGCTCTTCT 390
 DB 1 GTCTTTTCGCAATTACAGAGCTGACCTGGTATATPAAACAGTTTCAGGCTCTCTCT 60
 QY 391 ACTGCTGAAAGAGTGCTTAAGTGCTGTGTTAGTTGTATAGAAACAAATGCAATT 450
 DB 61 TCAGTATGAAAGAAATGGGTCAATGTGTATAGAGTTGGCATTTGAAGCTAATGCAATT 120
 QY 451 GTGCTGTTCATGATGATGAGATTGTACCAACCAAAATTTGAAAGAGCTGTACCTTTAC 510
 DB 121 ATCGCTGTTCCGTATGATTTGAGACTGCCCATCAATGCTTGAAGAGAGATCTGTAC 180
 QY 511 TTTCACAAGCTCAAGTT 527
 DB 181 TTTCACAAAATTAAAGTT 197

RESULT 9

ADP47831
 ID ADP47831 standard; DNA; 1872 BP.

AC ADP47831;

DT 26-FEB-2004 (first entry)

DE Schizosaccharomyces pombe acyltransferase DNA sequence SEQ ID NO:16.

KW acyltransferase; enzyme; membrane-spanning region;
 KM active membrane independent acyltransferase; fatty acid ester;
 KM fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol;
 KM phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;
 KM acylated amino acid; structured lipid; fat-soluble molecule; gene; ds.

XX Schizosaccharomyces pombe.

OS WO2003100044-A1.

PN 04-DEC-2003.

PD 28-MAY-2003; 2003WO-SE000870.

XX 29-MAY-2002; 2002SE-00001581.

PR 29-MAY-2002; 2002US-0383889P.

XX 20-JAN-2003; 2003SE-00000142.

PA (SCANBI) SCANDINAVIAN BIOTECHNOLOGY RES AB.

PI Dahlqvist A, Ghosal A, Lindqvist Y, Banas A;

XX WPI; 2004-053268/05.

DR P-PSDB; ADF47832.

XX New nucleotide sequence encoding an improved acyltransferase polypeptide,
 PT useful for producing structured lipids or fat-soluble molecules, in
 PT removing undesirable fat or in modifying lipids in animal or plant raw
 PT material.

PS Claim 5; SEQ ID NO 16; 91pp; English.

XX The present invention describes a nucleotide sequence (I) derived from a
 CC nucleotide sequence encoding an acyltransferase polypeptide comprising at
 CC least one membrane-spanning region. (I) encodes an improved active
 CC membrane independent acyltransferase polypeptide in which at least one
 CC amino acid residue of the membrane-spanning region has been deleted
 CC and/or substituted as compared to the original acyltransferase
 CC polypeptide, where the encoded active membrane independent
 CC acyltransferase polypeptide can produce fatty acid esters and/or fatty
 CC acid thioesters such as triacylglycerols, diacylglycerols,
 CC monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters,

CC acylated carbohydrates and acylated amino acids. Also described: (1) a
CC nucleotide sequence molecule (II) comprising at least one promoter region
CC which functions in a host, where the promoter region is operably linked
CC to at least one (I), which is operably linked to at least one non-
CC translated region which functions in a host; (2) a vector comprising (II)
CC; (3) a host cell comprising (II) or the vector; (4) producing an
CC improved active membrane independent acyltransferase polypeptide,
CC comprising providing the above host cell and a growth medium preparing a
CC host cell culture, culturing the host cell culture and harvesting the
CC host cell culture and recovering the improved active membrane independent
CC acyltransferase polypeptide; (5) a polypeptide obtained by the method in
CC (4), where the polypeptide at least is an improved active membrane
CC independent acyltransferase polypeptide; (6) an oligonucleotide
CC specifically hybridizing to (I) under stringent conditions; and (7) a kit
CC comprising the above polypeptide and a stabiliser. The nucleic acid
CC molecule (I) and the polypeptide are useful in producing structured
CC lipids or fat-soluble molecules, in removing undesirable fat or in
CC modifying lipids present in animal and plant raw material. The present
CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 1872 BP; 598 A; 297 C; 405 G; 572 T; 0 U; 0 Other;

XX Query Match 3.2%; Score 52.6; DB 12; Length 1872;

XX Best Local Similarity 47.4%; Pred. No. 3.6e-05;

XX Matches 157; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 420 TGTGATGTTGGTATAGAGCAATATGTCGCTGTTCCATGATGGAGATTGTC 479
DB 714 TGCTGCAATTTGGTTATAGAGCCTAATAACATGTTAGTGTTTTCATTTGGCGTTATTC 773
QY 480 ACCAACCAATTTGGAGAGCGGACCTTTACTTACAAAGCTCAAGTTGACCTTTGAAC 539
DB 774 ATATGCAATTTAGAGCAACGTAATAATTTTCAAAAGTTTCAAAAGTTTCAAGTA 833
QY 540 TGCTTAAACTCCGCGGCGCCCTTCTATAGTATTTGGCCATGATGGGTAATATGT 599
DB 834 CAGCAACATTTGACATAAGAAAAGAGTACTGTGATTTCTCACTCAAGGGTTCACAGT 893
QY 600 CTTGCAATCTTTCTGGAATGGCTAGAGGCTAGAAATGGCAACCAATTAATTGAAATG 659
DB 894 TACGACATATTTTAAAGTGGTGAAGCTAGAGGCTACGGAATGGTGACGACATTG 953
QY 660 GCTTATCAGCATATCCATGCTTATTGCGCTTTGAGAGCTCCTCTTCTTGGTTCTTGA 719
DB 954 GGTATATATATCATTTGGAAGCATTTATTAATATCGGATCTTGATTGGAGCACCGAA 1013
QY 720 GGCAATCAATCTACTCTCTGTGTGTAACG 750
DB 1014 AACAGTGGCAGCGCTTTATCGGGTGAATG 1044

XX RESULT 10

XX ADF47817 ID ADF47817 standard; DNA; 1701 BP.

XX AC ADF47817;

XX DT 26-FEB-2004 (first entry)

XX DE Yeast membrane independent acyltransferase DNA sequence SEQ ID NO:2.

XX acyltransferase; enzyme; membrane-spanning region;
XX active membrane independent acyltransferase; fatty acid ester;
XX fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol;
XX phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;
XX acylated amino acid; structured lipid; fat-soluble molecule; yeast; gene;
XX ds.

XX Saccharomyces cerevisiae.

XX OS MO2003100044-AL.

XX PN 04-DEC-2003.

XX PD

XX 28-MAY-2003; 2003WO-SE000870.

XX 29-MAY-2002; 2002SE-00001581.

XX 29-MAY-2002; 2002US-0383889P.

XX 20-JAN-2003; 2003SE-00000142.

XX (SCAN-) SCANDINAVIAN BIOTECHNOLOGY RES AB.

XX Dahlqvist A, Ghosal A, Lindqvist Y, Banas A;

XX WPI; 2004-053268/05.

XX New nucleotide sequence encoding an improved acyltransferase polypeptide,
XX useful for producing structured lipids or fat-soluble molecules, in
XX removing undesirable fat or in modifying lipids in animal or plant raw
XX material.

XX Claim 12, SEQ ID NO 2, 91pp; English.

XX The present invention describes a nucleotide sequence (I) derived from a
XX nucleotide sequence encoding an acyltransferase polypeptide comprising at
XX least one membrane-spanning region. (I) encodes an improved active
XX membrane independent acyltransferase polypeptide in which at least one
XX amino acid residue of the membrane-spanning region has been deleted
XX and/or substituted as compared to the original acyltransferase
XX polypeptide, where the encoded active membrane independent
XX acyltransferase polypeptide can produce fatty acid esters and/or fatty
XX acid thioesters such as triacylglycerols, diacylglycerols,
XX monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters,
XX acylated carbohydrates and acylated amino acids. Also described: (1) a
XX nucleotide sequence molecule (II) comprising at least one promoter region
XX which functions in a host, where the promoter region is operably linked
XX to at least one (I), which is operably linked to at least one non-
XX translated region which functions in a host; (2) a vector comprising (II)
XX; (3) a host cell comprising (II) or the vector; (4) producing an
XX improved active membrane independent acyltransferase polypeptide,
XX comprising providing the above host cell and a growth medium preparing a
XX host cell culture, culturing the host cell culture and harvesting the
XX host cell culture and recovering the improved active membrane independent
XX acyltransferase polypeptide; (5) a polypeptide obtained by the method in
XX (4), where the polypeptide at least is an improved active membrane
XX independent acyltransferase polypeptide; (6) an oligonucleotide
XX specifically hybridizing to (I) under stringent conditions; and (7) a kit
XX comprising the above polypeptide and a stabiliser. The nucleic acid
XX molecule (I) and the polypeptide are useful in producing structured
XX lipids or fat-soluble molecules, in removing undesirable fat or in
XX modifying lipids present in animal and plant raw material. The present
XX sequence is used in the exemplification of the present invention.

XX Sequence 1701 BP; 516 A; 317 C; 401 G; 467 T; 0 U; 0 Other;

XX Query Match 3.0%; Score 49.4; DB 12; Length 1701;

XX Best Local Similarity 49.2%; Pred. No. 0.00035;

XX Matches 162; Conservative 0; Mismatches 161; Indels 6; Gaps 1;

QY 428 TTGGTATAGAGCAATATGTCGCTGTTCCATGATGGAGATTGCACCAACA 487

DB 530 TTGGCTATGAAACCAATATAATGACAGTGTGGTATGATGGAGGCTTCATATTAG 589

QY 488 AATTGGAAGAGCGTACCTTTACTTTCAACAGCTCAAGTACCTTTAAACTGCTTAA 547

DB 590 ATCTAGAAAGACGGATAGTACTTTTCGAAAGCTTAAGAAACAAATCGAATGTTTCATC 649

QY 548 AACTCGGTGGGCGCTTCTATAGATTGGCCATTAAGGGTAATAATGCTTCAGAT 607

DB 650 AATTGAGTGGTGAAGAAAGTTGTTTAATTGACATTTCTATGGGTTCTAGATTAATCTTTT 709

QY 608 ACTTCTGGAATGGCTGAGGCTAGAAATGACCA-----AAACATTAATTGAGTGGC 661

DB 710 ACTTTAGAAATGAGGTGAGGCTGAGGCCCTTTACGGAATAGTGTGTGGCTGG 769

QY 662 TTGATCAGCATATCCATGCTTATTTCGCTGTGGAAGCTCTCTTCTTGGTTCTGTGAGG 721

Db 770 TTAAGCAACATGATTCATTCAATTAATGACGAGGACCGCTCTGGCGCTCCAAAG 829
 Qy 722 CAATCAATCTACTCTCTCTGCTGAAG 750
 Db 830 CAGTTCAGCTCTAATTAGTGTAATG 858

RESULT 11
 AAC64431
 ID AAC64431 standard; DNA; 1986 BP.

AC AAC64431;
 DT 12-FEB-2001 (first entry)
 XX Saccharomyces cerevisiae PDAT gene SEQ ID NO:1.

XX PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
 KW EST; expressed sequence tag; fatty acid; oil content; ds.
 XX Saccharomyces cerevisiae.

XX WO200060095-A2.
 PD 12-OCT-2000.

XX 28-MAR-2000; 2000WO-EP002701.

XX 01-APR-1999; 99EP-00106656.
 PR 10-JUN-1999; 99EP-00111321.
 PR 07-FEB-2000; 2000US-0180687P.

XX (BAD1) BASF PLANT SCI GMBH.

XX Dahlqvist A, Stahl U, Lenman M, Banas A, Ronne H, Stymne S;
 PI WPI; 2000-665012/64.
 DR P-PSDB; AAB24266.

XX Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
 PT pathway for triacylglycerol production and DNAs encoding them, useful for
 PT producing triacylglycerol, or for transforming any cell or organism to
 PT increase oil content.

XX Claim 6; Page 45-48; 97pp; English.

XX The present invention describes an enzyme for catalyzing (in an acyl-CoA-
 CC independent reaction) the transfer of fatty acids from phospholipids to
 CC diacylglycerol in the biosynthetic pathway for the production of
 CC triacylglycerol (TAG). The enzyme is designated as
 CC phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
 CC nucleotides encoding them are useful for producing TAG and/or TAG with
 CC uncommon fatty acids. The enzyme and the nucleotide are also useful for
 CC transforming any cell or organism in order to be expressed in this cell
 CC or organism and result in an altered, preferably increased oil content of
 CC this cell or organism. The present sequence encodes yeast (Saccharomyces
 CC cerevisiae) PDAT

XX Sequence 1986 BP; 615 A; 361 C; 478 G; 532 T; 0 U; 0 Other;

Qy Query Match 3.0%; Score 49.4; DB 3; Length 1986;
 Db Best Local Similarity 49.2%; Pred. No. 0.00039;
 Matches 162; Conservative 0; Mismatches 161; Indels 6; Gaps 1;

Qy 428 TTGGTATGAAGCAATGCAATGCTGCTGCTCATGATGAGATTGTCACCAACA 487
 Db 815 TTGGCTATGAAGCAATGCAATGCAATGCTGCTGCTCATGATGAGATTGAG 874
 Qy 488 AATTGGAAGAGCGGACCTTACTTTCAAGCTCAAGTGAATGACCTTTAA 547
 Db 875 ATCTAGAAAGAGCGGATGATGATTTAGCAAGCTTAAAGAAACAATGCAACTGTTTCATC 934

Qy 548 AACTCCGGGCGCCCTTCTAATAGTATTTGCCATTCATGAGGTAAATGCTTTCAAT 607
 Db 935 AATTGAGTGGAAGAAAGTTTGTATTATGACATTCATAGGGTTCAGATATCTTTT 994
 Qy 608 ACTTTCTGAATGGCTGAGGCTAAGTAATGACCA-----AATCATTTATTGAAGGCC 661
 Db 995 ACTTTATGAAGATGGGTGAGGCTGAGGCCCTCTTTACGGTAAATGAGTGGTGGG 1054
 Qy 662 TTGATCAGCATATCCATGCTTATTTGCTGTTGAGGCTCTCTTCTGTTCTGTTGAG 721
 Db 1055 TTAAGCAACATATGATTCATTATATGACAGAGGAGCGCTTCTGGCGCTCCAAAG 1114
 Qy 722 CAATCAATCTACTCTCTCTGCTGAAG 750
 Db 1115 CAGTTCAGCTCTAATTAGTGTAATG 1143

RESULT 12
 AAC64441
 ID AAC64441 standard; DNA; 1986 BP.

AC AAC64441;
 DT 12-FEB-2001 (first entry)

XX Saccharomyces cerevisiae PDAT gene SEQ ID NO:1b.

XX PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
 KW EST; expressed sequence tag; fatty acid; oil content; ds.
 XX Saccharomyces cerevisiae.

XX WO200060095-A2.
 PD 12-OCT-2000.

XX 28-MAR-2000; 2000WO-EP002701.

XX 01-APR-1999; 99EP-00106656.
 PR 10-JUN-1999; 99EP-00111321.
 PR 07-FEB-2000; 2000US-0180687P.

XX (BAD1) BASF PLANT SCI GMBH.

XX Dahlqvist A, Stahl U, Lenman M, Banas A, Ronne H, Stymne S;
 PI WPI; 2000-665012/64.
 DR P-PSDB; AAB24266.

XX Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
 PT pathway for triacylglycerol production and DNAs encoding them, useful for
 PT producing triacylglycerol, or for transforming any cell or organism to
 PT increase oil content.

XX Claim 6; Page 77-81; 97pp; English.

XX The present invention describes an enzyme for catalyzing (in an acyl-CoA-
 CC independent reaction) the transfer of fatty acids from phospholipids to
 CC diacylglycerol in the biosynthetic pathway for the production of
 CC triacylglycerol (TAG). The enzyme is designated as
 CC phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
 CC nucleotides encoding them are useful for producing TAG and/or TAG with
 CC uncommon fatty acids. The enzyme and the nucleotide are also useful for
 CC transforming any cell or organism in order to be expressed in this cell
 CC or organism and result in an altered, preferably increased oil content of
 CC this cell or organism. The present sequence represents the yeast
 CC (Saccharomyces cerevisiae) PDAT gene

XX Sequence 1986 BP; 613 A; 366 C; 479 G; 528 T; 0 U; 0 Other;

Qy Query Match 3.0%; Score 49.4; DB 3; Length 1986;
 Db Best Local Similarity 49.2%; Pred. No. 0.00039;
 Matches 162; Conservative 0; Mismatches 161; Indels 6; Gaps 1;

QY 428 TTGGTATGAAAGCAATGCAATTCCTGCTTTCATACGATTGAGATTGACCAACA 487
 DB 815 TTGGCTATGAAAGCAATGCAATTCCTGCTTTCATACGATTGAGATTGACCAACA 874
 QY 488 AATTGGAAGAGCGGTGACCTTTACTTTCAAGCTCAGGTGACCTTTGAAATGCTTTAA 547
 DB 875 ATCTGAAAGAGCGCATAGTACTTTAGAGAGCTTAAAGAACAAATCGAATGTTTCATC 934
 QY 548 AACTCCGTGGCGGCCCTTCTATAGTATTTGCCATTCATGGTAATAATGCTTCAGAT 607
 DB 935 AATTGAGTGGTGAAGAAAGTTTGTATTAATGACATTTATGGGTTCTCAGATTATCTTTT 994
 QY 608 ACTTCTGGAATGCTGAGGCTAGAAATGACCA-----AAACATTATTTGAAGTGC 661
 DB 995 ACTTTATGAAATGGGTGAGGCTGAAAGGCCCTTTACGGTAAATGTTGCTGCTGG 1054
 QY 662 TTGATCAGCATATTCATGCTTATTTCCGCTGTGAGCTCCTCTTGTGTTCTGTTGAG 721
 DB 1055 TTAAAGAACACATAGATTCATTTAATGACGACGAGGACGCTTGTGGCGCTCCAAAG 1114
 QY 722 CAATCAAACTACTCTCTCTGTGTGTAAG 750
 DB 1115 CAGTTCAGCTCTTACTTATGTTGTAAG 1143

RESULT 13

AAC64440
 ID AAC64440 standard; DNA; 1986 BP.

AAC64440;

12-FEB-2001 (first entry)

Saccharomyces cerevisiae PDAT ORF nucleotide sequence SEQ ID NO:4a.

KW PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
 KM EST; expressed sequence tag; fatty acid; oil content; ds.

XX Saccharomyces cerevisiae.

XX WO200060095-A2.

XX 12-OCT-2000.

XX 28-MAR-2000; 2000WO-EP002701.

XX 01-APR-1999; 99EP-00106656.

XX 10-JUN-1999; 99EP-00111321.

XX 07-FEB-2000; 2000US-0180687P.

XX (BADI) BASF PLANT SCI GMBH.

XX Dahlqvist A, Stahl U, Lenman M, Banas A, Ronne H, Stryme S;

XX WPI; 2000-665012/64.

XX P-PSDB; AAB24265.

XX Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic

XX pathway for triacylglycerol production and DNAs encoding them, useful for

XX increasing oil content.

XX Claim 6; Page 71-74; 97pp; English.

XX The present invention describes an enzyme for catalysing (in an acyl-CoA-

XX independent reaction) the transfer of fatty acids from phospholipids to

XX triacylglycerol (TAG). The enzyme is designated as

XX phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the

XX nucleotides encoding them are useful for producing TAG and/or TAG with

XX uncommon fatty acids. The enzyme and the nucleotide are also useful for

XX transforming any cell or organism in order to be expressed in this cell

CC or organism and result in an altered, preferably increased oil content of
 CC this cell or organism. The present sequence represents the yeast
 CC (Saccharomyces cerevisiae) PDAT ORF (open reading frame) nucleotide
 CC sequence
 XX

SQ Sequence 1986 BP; 615 A; 361 C; 478 G; 532 T; 0 U; 0 Other;

Query Match 3.0%; Score 49.4; DB 3; Length 1986;

Best Local Similarity 49.2%; Pred. No. 0.00039;

Matches 162; Conservative 0; Mismatches 161; Indels 6; Gaps 1;

QY 428 TTGGTATGAAAGCAATGCAATTCCTGCTTTCATACGATTGAGATTGACCAACA 487
 DB 815 TTGGCTATGAAAGCAATGCAATTCCTGCTTTCATACGATTGAGATTGACCAACA 874
 QY 488 AATTGGAAGAGCGGTGACCTTTACTTTCAAGCTCAGGTGACCTTTGAAATGCTTTAA 547
 DB 875 ATCTGAAAGAGCGCATAGTACTTTAGAGAGCTTAAAGAACAAATCGAATGTTTCATC 934
 QY 548 AACTCCGTGGCGGCCCTTCTATAGTATTTGCCATTCATGGTAATAATGCTTCAGAT 607
 DB 935 AATTGAGTGGTGAAGAAAGTTTGTATTAATGACATTTATGGGTTCTCAGATTATCTTTT 994
 QY 608 ACTTCTGGAATGCTGAGGCTAGAAATGACCA-----AAACATTATTTGAAGTGC 661
 DB 995 ACTTTATGAAATGGGTGAGGCTGAAAGGCCCTTTACGGTAAATGTTGCTGCTGG 1054
 QY 662 TTGATCAGCATATTCATGCTTATTTCCGCTGTGAGCTCCTCTTGTGTTCTGTTGAG 721
 DB 1055 TTAAAGAACACATAGATTCATTTAATGACGACGAGGACGCTTGTGGCGCTCCAAAG 1114
 QY 722 CAATCAAACTACTCTCTCTGTGTGTAAG 750
 DB 1115 CAGTTCAGCTCTTACTTATGTTGTAAG 1143

RESULT 14

AAS01342
 ID AAS01342 standard; DNA; 1986 BP.

AAS01342;

31-MAY-2001 (first entry)

DE Yeast LCAT related open reading frame 1 (LRO1) gene.

KW Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;

KW acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;

KW nutritional supplement; dairy product; food product; salad dressing;

KW yeast; Arabidopsis thaliana; LCAT related open reading frame 1; LRO1; ds.

XX Saccharomyces cerevisiae.

XX Key Location/Qualifiers

XX CDS 1..1986

XX FT /*tag= a

XX FT /product= "LRO1"

XX MO200116308-A2.

XX 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US023863.

XX 30-AUG-1999; 99US-0152493P.

XX (MONS) MONSANTO CO.

XX Laessner M, Van Bennaam A;

XX WPI; 2001-169010/17.

XX P-PSDB; AAU00464.

PT New isolated nucleic acid encoding plant lecitlin:cholesterol
 PT acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase
 PT -like polypeptides, for modifying the sterol content and oil production
 PT of plants.

PS Claim 5, Page 116-117, 127pp, English.

XX The present sequence encoding for yeast LCAT related open reading frame,
 XX (LRO1) is described in an invention relating to several novel
 CC polynucleotides encoding the plant sterol acyltransferases LCAT
 CC (lecithin:cholesterol acyltransferase-like; AA001081-AA01104, AA01341)
 CC and ACAT (acyl CoA:cholesterol acyltransferase-like; AA01311-AA01313).
 CC A rat ACAT-like cDNA sequence (AA01105) is also described. The
 CC polynucleotides encoding LCAT or ACAT are used to produce LCAT or ACAT
 CC polypeptides. They can also be used in a recombinant construct to
 CC transform a host cell (preferably of a plant) or a plant. The recombinant
 CC construct is used to increase or decrease the sterol content of the host
 CC cell or plant. It can be used to alter oil production of the cell or
 CC plant, preferably by increasing it. The oil of the plant or the plant
 CC itself is used as a food product, or as nutritional or dietary
 CC supplements, or in pharmaceutical compositions for lowering cholesterol.
 CC The oil can be used in foods e.g. margarine, butter, cooking oil, and
 CC dressings e.g. salad dressings, mayonnaise, cheese, processed meat,
 CC pasta, sauces, cereals, desserts, dips, chips, baked goods, pastries,
 CC cookies, snack bars, confections, chocolates, and beverages. The
 CC alteration in sterol content and/or composition can also provide a plant
 CC with tolerance to stress and insect damage

XX Sequence 1986 BP, 615 A, 361 C, 478 G, 532 T, 0 U, 0 Other;

SO Query Match 3.0%; Score 49.4; DB 5; Length 1986;

Best Local Similarity 49.2%; Pred. No. 0.00039;

Matches 162; Conservative 0; Mismatches 161; Indels 6; Gaps 1;

Qy 428 TTGGTATGAGCAAAATGCAATGTCGCTGTTCCATGAGTGGAGATTGCACCA 487
 Db 815 TTGGCTATGAAACCCAAATAAATGACGAGTGTGCTGATGATGAGGCTTCATATTAG 874
 Qy 488 AATTGGAAGAGCGGACCTTACTTCAAGCTCAATGTAACCTTGAACGTGTTAA 547
 Db 875 ATCTGAAAGAGCGCATAGTACTTACGAAGCTTAAGAAACAATGCAACTGTTATC 934
 Qy 548 AACTCGTGCGGCGCTTCTATAGTATTGGCCATTCAATGGTAAATGCTTCAAT 607
 Db 935 AATTGAGTGGTGAAGAAATGTTGTTAATGAGCAATTCATGAGTTCAGATTAATCTTT 994
 Qy 608 ACTTTTGGAAATGCTGAGCTAGAAATTGACCA-----AAACATTATTGAATGGC 661
 Db 995 ACTTTATGAAATGGGTGAGGCTGAAAGCCCTCTTTACGTAATGCTGCTGCTGGG 1054
 Qy 662 TTGATCGCATATCCATGCTATTTCGCTGTTGAGCTCCTCTTCTTGGTCTGTGAG 721
 Db 1055 TTAACGAAACATGATTCATTCAATTAAGACGAGGACCTTCTGCGCCCTCCAAAG 1114
 Qy 722 CAATCAATCTACTCTCTCTGTGTAAG 750
 Db 1115 CAGTTCAGCTCTAATTAGTGTGAATG 1143

RESULT 15

ADP47816 ID ADF47816 standard; DNA; 1986 BP.

XX ADF47816;

XX 26-FEB-2004 (first entry)

XX Yeast acyltransferase nucleotide sequence SEQ ID NO:1.

KW acyltransferase; enzyme; membrane-spanning region;
 KW active membrane independent acyltransferase; fatty acid ester;
 KW fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol;
 KW phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;

KW acylated amino acid; structured lipid; fat-soluble molecule; yeast; gene;
 KW ds.

OS Saccharomyces cerevisiae.

XX WO2003100044-A1.

XX 04-DEC-2003.

XX 28-MAY-2003; 2003WO-SB000870.

XX 29-MAY-2002; 2002SE-00001581.

XX 29-MAY-2002; 2002US-0383889P.

XX 20-JAN-2003; 2003SE-00000142.

XX (SCAN-) SCANDINAVIAN BIOTECHNOLOGY RES AB.

XX Dahlqvist A, Ghosal A, Lindqvist Y, Banas A;

XX WPI; 2004-053268/05.

XX P-PSDB; ADF47818.

PT New nucleotide sequence encoding an improved acyltransferase polypeptide,
 PT useful for producing structured lipids or fat-soluble molecules, in
 PT removing undesirable fat or in modifying lipids in animal or plant raw
 PT material.

XX Claim 5; SEQ ID NO 1; 91pp; English.

XX The present invention describes a nucleotide sequence (1) derived from a
 CC nucleotide sequence encoding an acyltransferase polypeptide comprising at
 CC least one membrane-spanning region. (1) encodes an improved active
 CC membrane independent acyltransferase polypeptide in which at least one
 CC amino acid residue of the membrane-spanning region has been deleted
 CC and/or substituted as compared to the original acyltransferase
 CC polypeptide, where the encoded active membrane independent
 CC acyltransferase polypeptide can produce fatty acid esters and/or fatty
 CC monoacylglycerols, phospholipids, glycolipids, diacylglycerols,
 CC monoacylglycerols, phospholipids, lysolipids, waxes, waxes, waxes,
 CC acylated carbohydrates and acylated amino acids. Also described: (1) a
 CC nucleotide sequence molecule (1) comprising at least one promoter region
 CC which functions in a host, where the promoter region is operably linked
 CC to at least one (1), which is operably linked to at least one non-
 CC translated region which functions in a host; (2) a vector comprising (1)
 CC (3) a host cell comprising (1) or the vector; (4) producing an
 CC improved active membrane independent acyltransferase polypeptide,
 CC comprising providing the above host cell and a growth medium preparing a
 CC host cell culture, culturing the host cell culture and harvesting the
 CC host cell culture and recovering the improved active membrane independent
 CC acyltransferase polypeptide; (5) a polypeptide obtained by the method in
 CC (4), where the polypeptide at least is an improved active membrane
 CC independent acyltransferase polypeptide; (6) an oligonucleotide
 CC specifically hybridizing to (1) under stringent conditions; and (7) a kit
 CC comprising the above polypeptide and a stabiliser. The nucleic acid
 CC molecule (1) and the polypeptide are useful in producing structured
 CC lipids or fat-soluble molecules, in removing undesirable fat or in
 CC modifying lipids present in animal and plant raw material. The present
 CC sequence is used in the exemplification of the present invention.

XX Sequence 1986 BP, 615 A, 361 C, 478 G, 532 T, 0 U, 0 Other;

SO Query Match 3.0%; Score 49.4; DB 12; Length 1986;

Best Local Similarity 49.2%; Pred. No. 0.00039;

Matches 162; Conservative 0; Mismatches 161; Indels 6; Gaps 1;

Qy 428 TTGGTATGAGCAAAATGCAATGTCGCTGTTCCATGAGTGGAGATTGCACCA 487
 Db 815 TTGGCTATGAAACCCAAATAAATGACGAGTGTGCTGATGATGAGGCTTCATATTAG 874
 Qy 488 AATTGGAAGAGCGGACCTTACTTCAAGCTCAATGTAACCTTGAACGTGTTAA 547
 Db 875 ATCTGAAAGAGCGCATAGTACTTACGAAGCTTAAGAAACAATGCAACTGTTATC 934


```
QY 548 AACGCCGCGCGCCCTTCTATAGTATTGCGCCATTCAATGGTAAATGCTTCAGAT 607
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Db 935 AATTGAGTGGTGAAGAAAGTTGTTAAATTGACATTCTATGGTCTCAGATTATCTTTT 994
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QY 608 ACTTCTGGAATGGCTGAGGCTAGAAATTGCACA-----AAACATTATTGAAGTGC 661
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Db 995 ACTTATGAAATGGTCAAGGCTGAAGGCCCTCTTTACGTAATGAGTGTCTGTGGCTGG 1054
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QY 662 TTGATCAGCATAATCCATGCTTAATTCGCTGTGAGACTCTCTTCTTGGTTCTGTTGAG 721
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Db 1055 TTAACGAACACATAGATTCAATCATTAATGACAGGAGCGGCTTCTGGCGCTCCAAAG 1114
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QY 722 CAATCAAACTTACTCTCTCTGTGTAAAG 750
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1115 CAGTTCAGCTCTAATTAGTGTGAATG 1143
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Search completed: November 8, 2004, 22:55:43
Job time : 840 secs

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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 22:37:51 ; Search time 5402 Seconds
(without alignments)
11069.530 Million cell updates/sec

Title: US-09-651-651-4
Perfect score: 1 atggagcgcgaattcgaattc.....ctgataaagtggtatcaa 1641
Sequence:

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

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1: gb_eest1:
2: gb_eest2:
3: gb_hcc1:
4: gb_eest3:
5: gb_eest4:
6: gb_eest5:
7: gb_eest6:
8: gb_gsest1:
9: gb_gsest2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	484	29.5	596	1	AU237072 AU237072
2	464.2	28.3	596	7	CK259394 EST705472
3	438.8	26.7	752	7	CF844688 P8H8029XF
4	397	24.2	713	7	CK319714 CGF100474
5	386.2	23.5	788	7	CK259393 EST705471
6	376.8	22.0	666	7	CK260764 EST706842
7	374.8	22.8	686	5	BO508623 EST616038
8	367	22.4	792	4	BG600021 EST504916
9	350.8	21.4	565	5	BO584361 E011859-0
10	343	20.9	560	6	CD710878 VVA026C02
11	331.8	20.2	676	6	CA090564 SCGAM210
12	316.4	19.3	534	6	AI974291 T1102936
13	306.6	18.7	628	4	BI267124 NF097C071
14	293.4	17.9	728	1	AU206500 AU206500
15	291.8	17.8	683	6	CA221313 SCSEFL403
16	268.8	16.4	647	6	CA156623 SCSEFL308
17	266.6	15.8	502	7	CK115712 Y014D01 P
18	208.6	12.7	394	1	AU290926 AU290926
19	207.6	12.7	704	4	BI422757 EST533423
20	206.2	12.6	488	4	BI267156 NF101G041
21	189.2	11.5	792	4	BG367066 HVSME1001
22	185	11.3	632	4	BI922233 EST542136
23	182.2	11.1	559	2	AW760400 g149G03.Y
24	180.4	11.0	518	2	BE321377 NF042H091

25	176.8	10.8	666	8	BH974706
26	168.6	10.3	698	7	CO532456
27	167.6	10.2	1225	8	BI11175
28	165.6	10.1	625	8	BH944186
29	160.2	9.8	692	7	CO521704
30	160	9.8	542	2	AM120335
31	159	9.7	840	7	CK260765
32	137	8.3	582	1	AU287072
33	135.2	8.2	207	8	BH746163
34	134.8	8.2	503	4	BI595853
35	133.4	8.1	303	8	BH548609
36	133.4	8.1	737	1	AT611569
37	126.6	7.7	493	9	CC948076
38	123.8	7.5	546	9	CC948085
39	122.4	7.5	486	1	AT771341
40	122.4	7.5	496	1	AT488511
41	122.4	7.5	709	1	AT488635
42	118.6	7.2	429	1	AT488359
43	113.2	6.9	967	8	CC373126
44	106.2	6.5	579	7	CO722489
45	104.8	6.4	712	4	BI932257

ALIGNMENTS

RESULT 1
LOCUS AU237072 596 bp mRNA linear EST 01-APR-2002
DEFINITION AU237072 RAF15 Arabidopsis thaliana cDNA clone RAF15-47-A08 5',
mRNA sequence.
ACCESSION AU237072
VERSION AU237072.1 GI:19876241
KEYWORDS EST.

SOURCE Arabidopsis thaliana (chale crese)
ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 596)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawar,U.,
Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A.,
Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)

TITLE JOURNAL
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msekic@rcc.riken.go.jp

FEATURES
source location/Qualifiers
1..596
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAF15-47-A08"
/cbase="RAF15-47-A08"
/lab_host="mixture of salique and flower"
/clone_lib="DH10B"
/note="Site_1: BamHI, Site_2: SalI"

ORIGIN
Query Match 29.5%; Score 484; DB 1; Length 596;

Best Local Similarity 99.4%; Pred. No. 9,9e-134;
Matches 484; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGAGGCAATTCGAAATCAGTAACGGCTTCTTCAACGGTATCGCGGTTTTTTCTTG 60
DB 110 ATGGAGGCAATTCGAAATCAGTAACGGCTTCTTCAACGGTATCGCGGTTTTTTCTTG 169
QY 61 ATTTCGGGTGGCCGAACCTGCGGTGAGATGAGACCGAGTTTCACGGGACTACTCGAAG 120
DB 170 ATTTCGGGTGGCCGAACCTGCGGTGAGATGAGACCGAGTTTCACGGGACTACTCGAAG 229
QY 121 CTATGGGGATATATATTCGGGATTTGGCTGAGACGAGCTAGCGGTGCTGATCTT 180
DB 230 CTATGGGGATATATATTCGGGATTTGGCTGAGACGAGCTAGCGGTGCTGATCTT 289
QY 181 GACTGTCCATACACTCCGTTGAGCTTCAATCCGCTGACCTGATGAGTGGCTAGACCACT 240
DB 290 GACTGTCCATACACTCCGTTGAGCTTCAATCCGCTGACCTGATGAGTGGCTAGACCACT 349
QY 241 AAGCTTCTTTCTGCTGCTCAACTGCTGTTTAAAGTATAGTGTGCTAATCTTATATCAA 300
DB 350 AAGCTTCTTTCTGCTGCTCAACTGCTGTTTAAAGTATAGTGTGCTAATCTTATATCAA 409
QY 301 ACAGACCATCCCGAGTGAAGTACAGGCTGACAGTGTCTTTGACCATGACAGAAATG 360
DB 410 ACAGACCATCCCGAGTGAAGTACAGGCTGACAGTGTCTTTGACCATGACAGAAATG 469
QY 361 GATCCAGGTTACATTAACAGTCTCTTTCTAAGTCTGAGAAAGAGTGGCTTAAGTGTGT 420
DB 470 GATCCAGGTTACATTAACAGTCTCTTTCTAAGTCTGAGAAAGAGTGGCTTAAGTGTGT 529
QY 421 GTTGAGTTTGTATGAAGCAATGCAATGTGCTGTTCCATGCAATGAGATGTCA 480
DB 530 GTTGAGTTTGTATGAAGCAATGCAATGTGCTGTTCCATGCAATGAGATGTCA 589
QY 481 CCAACCA 487
DB 590 CCAACCA 596

RESULT 2
CK259394
LOCUS CK259394 946 bp mRNA linear EST 03-AUG-2004
DEFINITION EST705472 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAB029 5' end, mRNA sequence.
ACCESSION CK259394
VERSION CK259394.1 GI:39816372
KEYWORDS EST
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 946)
Buell, C.R., Hart, A., Ziemann, V., Kazymycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST705470 EST705471 EST705473
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: CAG GAA ACA GCT ATG ACC.

FEATURES
source
1..946
/organism="Solanum tuberosum"
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAB029"
/tissue_type="abiotic stress treated leaf and root tissue"

/lab_host="DH10B-TonA"
/clone_id="potato abiotic stress cDNA library"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d, and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN
Query Match 28.3%; Score 464.2; DB 7; Length 946;
Best Local Similarity 70.7%; Pred. No. 1.1e-127;
Matches 671; Conservative 0; Mismatches 253; Indels 25; Gaps 3;

QY 678 TGCCTAATTTGCTGTGAGAGCTCTCTTCTTGTGTTGAGCAATCAATCTACTCT 737
DB 1 TGCCTAATTTGCTGTGAGAGCTCTCTTCTTGTGTTGAGCAATCAATCTACTCT 60
QY 738 CTCTGTGTAACTTTGGCCCTTCCTGTTCTGAGGAACTGCTGGTGTGCTCAATTC 797
DB 61 ATCGGGGTCTTACATTTGCTCTCTCTGTTTCAAGGGGACAGCTGCCGATGTTCAATAC 120
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QY 858 CTGAGCCATTTTCTGAGGGGTGCTGCAAAAGAAATAGCGGTATACCATCTGTATGA 917
DB 181 TCGGAGCATTTCTCT---GGTGAACAAGAAATATACCATCTCTACCATCTCGATGA 237
QY 918 AGAGGAATATCAATCAAAATATCTGCTGCGGCAAAATATTTTAACTTGAATTC 977
DB 238 GCATGAACCTTAATCAAAAGTACTGTGGCTGCAAAACATTAATCAATGAAATTC 297
QY 978 TTCCACTAG-----CGTTACAGAAACAGCTCTAGTCAACATGAC 1016
DB 298 TTTCATTTGAGGAAATAGAGTTTATCCCTCAGTTGTGAAACCTGCCAAACCACTTGTG 357
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DB 358 TGAATGAATGTGATTTCCGACACAAATGTCTTTTCTGCTGTGAAGTCTGTGACGG 417
QY 1077 GACTCTTTTCAAGCAATTAAGACTATGACCCGAGATGAGAGATGTATACCCAGTT 1136
DB 418 AACCTTTTCAAAACCAATTAAGATTTATGATCTGAGACGTAAGAACTCTTTCACCTTTT 477
QY 1137 AAAGAGTTGATCATGATGACCTGTTTTTAACTCTGCTGACTCTTGGAGAGACCAACC 1196
DB 478 AAAAAGTCTTACATATGATGATCGATTTTAAATCTCTTAAACCTTGGGAAACACACC 537
QY 1197 TATTAATAATGATTTGCAATATATGTGCTCATTAAGACAGAGGTGTATTAATT 1256
DB 538 TCTCAAGACATATTTGCAATTTATGCGTAGATTCAAGACTGAGGTTGGTACTATTT 597
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Db 598 TGACCAAGTGGAGAGCTTATCTCGATTAATTGATTATTAACAGATGTGATATATGAAT 657
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Qy 1377 TGGGAGATGAGACGGTACCTTATCACTCTCTGTGTGCAAGAAATTGGCTCGACCTTA 1436
Db 718 TGGGAGATGAGACGGTACCTTATCACTCTCTGTGTGCAAGAAATTGGCTGGGGCCAAA 777
Qy 1437 AGTTAACAATAAATGCTGCCCAAGCAAGAACAGATGAAAGCAAGTATGTGAACCT 1496
Db 778 AGTAAACATAACAAGAACCAAGTCAAGACATGATGCTCAGCTGTAAAGTGCATCA 837
Qy 1497 AATGTTGATCAT-GAGCATGGGTGAGACATCATATGATGACAAAGCAACCAAGG 1555
Db 838 AATATATGAGCATCCACATGATGTGAGATATCATTTCCCAATATGCAAAAGTTAGTACA 897
Qy 1556 TTAAGTACATAACCTTTTATGAGACATCTGAGAGCATTCGGGGAGAG 1604
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RESULT 3
CF844688 752 bp mRNA linear EST 30-OCT-2003
LOCUS pshB029xp13f USDA-IRAPS:Expression of Phytophthora sojae genes during infection and propagation_shB Phytophthora sojae cDNA clone SHB029F13 5, mRNA sequence.
ACCESSION CF844688 GI:38060342
VERSION CF844688
KEYWORDS EST.
SOURCE Phytophthora sojae
ORGANISM Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Phytophthora.
1 (bases 1 to 752)
REFERENCE Tyler B. Not Published
AUTHORS Tyler B. Not Published
TITLE Unpublished (2003)
JOURNAL Contact: Tyler B
COMMENT Tyler lab
VBI
1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtcyler@vt.edu
PCR Primers
FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 029 row: F column: 13
Seq primer: BK reverse primer
High quality sequence stop: 752.
Location/Qualifiers
1..752
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="SHB029F13"
/tissue_type="mycelium"
/cell_line="P6497"
/dev_stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone_id="USDA-IRAPS:Expression of Phytophthora sojae genes during infection and propagation_shB"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 26.7%; Score 438.8; DB 7; Length 752;
Best local similarity 79.9%; Pred. No. 4,4e-120;
Matches 526; Conservative 0; Mismatches 131; Indels 1; Gaps 1;
Qy 108 CGACTACTCGAAGCTATCGGATATATCATTTCCGGATTTGCTGACGACGACTACGAGC 167
|||||

Db 94 CGACTACTCGAAGCTATCCGGCATTAATATCCCTGGCTTGGCATCACTACGCTCCGAGC 153
Qy 168 GTGGTCATCTCTGATCTGTCATACATCCGTTGGAATTCATCCGCTGACCTGATG 227
Db 154 ATGGTCATTTTCATCTGATCTCTGATCTGATCTGATCTGATCTGATCTGATCTG 213
Qy 228 GCTAGACACCACTAAGCTCTTTCTGCTGTCACATGCTGTTAAGTATGTGCTAGA 287
Db 214 GCTGACACCAACCAACTCTTTCTGCTGTCATATGCTGCTTAAGTATGTGCTAGA 273
Qy 288 TCCTTATATATAACAGACATCCCGAGTGAATGTCAGGCTGACAGTGTCTTTGAGC 347
Db 274 TCCTTACATACAGACATCTGATGTGAATGCTGCTGATGTGTGCTTTCTGG 333
Qy 348 CATCACGAATTTGATCAGGTTACATTAACAGTCTCTTTCTAATGCTGGAAGAGTG 407
Db 334 TATTACGAATTTTATCCGGTATATATACAGACCTTTTCATCGGTTGGAAGATG 393
Qy 408 GCTTAAGTGTGTGTTGATGTTGATATAGAAAGCAATGTGCTGTTTCATAGA 467
Db 394 GATTAAAGTGTGATTTGATTTGGCATAGAAAGTAAATGATTTGCTGTTCCATAGA 453
Qy 468 TTGAGATTTGTCACCAACCAATGGAAGAGCGTGAAGCTTACTTTCACAGCTCAAGT 527
Db 454 TTGAGATTTGTGCGCTTCACAGCTTGAAGAGCGGAGCTTACTTTCATAGCTAAAGAT 513
Qy 528 GACCTTGAACCTGCTTAAAGCTCCGTCGCGGCTTCTATAGATTTGGCCATTCAT 587
Db 514 AACATTTGAACCTGCTTAAAGCTCCGTCGCGGCTTCTATAGATTTGGCCATTCAT 573
Qy 588 GGTATATATGCTCTTCAATCTTCTGATCTTCTGATGCTGAGCTGAGTAAATGCAACAAACA 647
Db 574 GGTATATATGCTTTCGCTTATTTCTGAGATGTTGAGTAAAGATGCAACAAACA 633
Qy 648 TTATTTGAAGTGTGCTT-GATGACATATTCATGCTTATTTGCTGTTGAGCTCTCTTC 706
Db 634 TTATATCCAGTGGGTGATCAATATTCCTGCTTATTTGCTGTTGAGCTCTCTTC 693
Qy 707 TTGTTCTGTTGAGGCAATCAATCTCTCTGCTGATGCTTGGCTTCTCTGT 764
Db 694 TTGTTCTGTTGAGGCAATCAATCTCTCTGCTGATGCTTGGCTTCTCTGT 751

RESULT 4
CK939714 713 bp mRNA linear EST 19-MAR-2004
LOCUS CDF1004746_F04 Developing fruit flavedo at 165 DABP Citrus sinensis cDNA clone F1650002_1IF_F04 5', mRNA sequence.
ACCESSION CK939714
VERSION CK939714.1 GI:45452970
KEYWORDS EST.
SOURCE Citrus sinensis
ORGANISM Citrus sinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroside II; Sapindales; Rutaceae; Citrus.
1 (bases 1 to 713)
REFERENCE Urtasu, S., Beek, J., Leelle, A., Xu, J., Cook, D. and Dandekar, A. Analysis of peel specific genes in Citrus (2004)
JOURNAL Unpublished (2004)
CONTACT: Abhaya Dandekar, PhD
COMMENT CAES Genome Facility
UC Davis, Department of Pomology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 752 7784
Fax: 530 752 8502
Email: amdandekar@ucdavis.edu
Seq primer: MSC-F-TCCGAGTCTGACGAGC.
Location/Qualifiers
1..713
/organism="Citrus sinensis"
/mol_type="mRNA"
/cultiivar="Washington navel orange"

FEATURES
Source


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Qy 797 CTTTGGCTGCTCATTTGGCTTATGACATTTTCAAGAAATGCAAGGTGATACACAT 856
Db 121 CATTTGATCTCTATATGATGATGATACATTTTCAAAATATTTGACAACTGATATGAT 180
Qy 857 CTTGAGCAGCATTTTTCGGGGGCTGCAAGAAAGATAGCCGGTATACCATGTGATG 916
Db 181 ATCCGAGACATTTCTCT---GGTGAACAAGAAAATACATCATGCTTACCATGCGATG 237
Qy 917 AAGAGAAATATCATTAATAATATCTGGCTGCGGACAAATATATTATTAACATTTAAATTC 976
Db 238 AGCATGAATTAATTAATCAAAAGTACTGCTGCTGCGCAACAAATATATCAATTTGAAGTTC 297
Qy 977 CTTTCACTAGT-----CGTTACAGAAACAGCTTACTAGTCAACATGA 1015
Db 298 CTTTGATTCGAGGAAATGAGTTTATCCCTCAAGTTGTAAGAACTGCCAAACCAACTTGT 357
Qy 1016 CCAGCATGGAATGTGGCCCTTCCACCCCTTTTGTCTTTCACAGCCCGTGAACCTAGCAATG 1075
Db 358 CTGGAATGGAATGTGATTCCTCCGACACAAATGTCTTTTCTGTGTAAGTCTCTGACG 417
Qy 1076 GGACTCTTTTCAAGCAATAGAACATTAACCTGACCCAGATAGCAAGAGATTTACACCACT 1135
Db 418 GAACCTTTTCAAGCCATAAGAAATTAATGATCTGACAGTGAAGAACTCTTTGACCTTT 477
Qy 1136 TAAAGAAATGATCATGATGATGACCTGTTTAAATCCTGATCTCTTGGAGAGACAC 1195
Db 478 TAAAGAAATCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
Qy 1196 CTATTAATAAATGATTTTGTGATATATGTGCTCATCTAAGACAGAGGTGATTAATCT 1255
Db 538 CTCTCAAGAACATATTTGATGATATGATGATGATGATGATGATGATGATGATGATGAT 597
Qy 1256 TTGCCCCCAAGGCAAACTTATCTGATATATGATGATGATGATGATGATGATGATGAT 1315
Db 598 TTGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 657
Qy 1316 CTGAGAGTTCCCTGCTGCAAGTCTGGAAGTGTGATGATGGAAGCTGGAACCTATTA 1375
Db 658 TCGAAGGATCTCTGATTTCCCGTCAAGAAATGTGTTGAAGAAACCTGTGTCACAA 717
Qy 1376 CTGGGAGTGAAGCGTACCTATCATTTGATCTCTTGGTGCAAGATTTGGTGGAGCTTA 1435
Db 718 GTGGGAGTGAAGCGTGGCTATCATCTCTCTCTGTCAGAAATTTGGTGGAGCTTA 777
Qy 1436 AAGTTACATA 1446
Db 778 AAGTGAACATA 788

RESULT 6
CK260764 968 bp mRNA linear EST 03-AUG-2004
LOCUS EST706842 potato abiotic stress cDNA library Solanum tuberosum cDNA
DEFINITION clone FOAB552 5' end, mRNA sequence.
ACCESSION CK260764
VERSION CK260764.1 GI:39817742
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 968)
Buell, C.R., Hart, A., Zismann, V., Karameycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST706843
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics

```

Institute via <http://genome.arizona.edu/orders/>
 Seq primer: ATT TAG GTG ACA CTA TAG.
 Location/Qualifiers
 1..968

FEATURES
 source
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultiivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="FOAB552"
 /clone_type="abiotic stress treated leaf and root tissue"
 /lab_host="DH10B-Tona"
 /clone_id="Potato abiotic stress cDNA library"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, 1d, 2d, and 4d; leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Query Match 23.0%; Score 376.8; DB 7; Length 968;
 Best Local Similarity 74.1%; Pred. No. 2.2e-101;
 Matches 477; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

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Qy 988 GTTACAGAAACAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1047
Db 22 GTTGTAGAAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 81
Qy 1048 TCTTTACAGCCCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1107
Db 82 TCTTTTCTGCTGAGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 141
Qy 1108 CCAGATGACAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1167
Db 142 CTGACAGTGAAGAGCTCTTCACTTTTAAAAAGCTTACATGATGATGATGATGATGAT 201
Qy 1168 AATCTCTGACTCTTGGAGAGACCACTATTAATAAATGATTTTGCATATATGCTGCT 1227
Db 202 AATCCTTAACACCTTGGAGAAAGACCACTCTCAAGAAATATCTGCATTTATGGCGTA 261
Qy 1228 CATCTAAGACAGAGTTGATTTACTTTGCCCAAGTGCACAACTTATCCGATTAAT 1287
Db 262 GATTGGAAGACTGGGTTGTTACTATTTTGCACCAAGTGGAAAGCTTATCTGATTAAT 321
Qy 1288 TGATCATCAAGATATCATTTAGAAATGAAAGTTCCTCGTGTCAAGCTGTGAAGT 1347
Db 322 TGATTTAACAAGATGATATGAAATGAAAGATCTCTGATTTCCGGTCAAGAAAT 381
Qy 1348 GTGGTGAATGGAAGCTGTGACCTATTAATCTGGGATGATGACGATACCTATTCATC 1407
Db 382 CTGGTTGAAGAAACCTGTGGTCAACAAGTGGGATGATGACGATGATACCATTTCCCTC 441
Qy 1408 TCTTGTGCAAGAAATTTGGCTCGGACCTAAGTTAACAATAGGCTCCCGCCAGCAAA 1467
Db 442 TCTGTGCAAGAAATTTGGCTCGGAGCCAAAAGTGAACATTAACAGAGACCAACAGTCA 501

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Qy 1468 CACGATGGAAGCAGCTCATGTGTAACCTTAATGTTGATCATGACATGGCTGACATC 1527
 Db 502 CATGATGGCTCAGCGCTGATCAAGTGCATCAAAATATAGAGCATCAACATGGTGAATATC 561
 Qy 1528 ATAGCTACATGACAAAAGCAACCAAGGGTTAGTACATACCTTTTATGAGAGCTTGAG 1587
 Db 562 ATCCCAATATGACAAAGTTAGCTTCAATGAGTACATGACCTTATTTATGAGGATTTGAA 621
 Qy 1588 AGCATTCGGGGGAGAGAACCGCACTGTGGAGCTTGATTAAG 1631
 Db 622 AGTTTCCAGGAACGAGAACAGCAGTTGGAGCTTGATTAAG 665
 RESULT 7
 LOCUS BQ508623 686 bp mRNA linear EST 07-MAR-2003
 DEFINITION EST616038 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMGX37 5', end, mRNA sequence.
 ACCESSION BQ508623
 VERSION BQ508623.2 GI:21924395
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum.
 Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Reiter, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karanymcheva, S.A.
 Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)
 On Jun 10, 2002 this sequence version replaced gi:21367492.
 Other ESTs: EST616039
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
 http://genome.arizona.edu/orders/
 Seq primer: T3.
 Location/Qualifiers
 1..686
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec or Binjete"
 /db_xref="taxon:4113"
 /clone="STMGX37"
 /tissue_type="mixed tissues"
 /lab_host="SOLR"
 /clone_1ib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
 /note="Vector: pBluescript SK(-), Site 1: EcoRI, Site 2: XhoI; supplier: Combination of untreated and Phytophthora infestans-created libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."
 ORIGIN
 Query Match 22.8%; Score 374.8; DB 5; Length 686;
 Best Local Similarity 74.0%; Pred. No. 7.6e-101;
 Matches 475; Conservative 0; Mismatches 167; Indels 0; Gaps 0;
 Qy 988 GTTACAGAAACGCTCTAGTCAATGACGACGATGATGGCTCCGACCTTTTG 1047
 Db 4 GTTGAGAACTGCCCCAAACCACTTGTCTGAAATGAGATGATTTCCGACAAATTTG 63
 Qy 1048 TCTTTCACAGCCCGCTGAACTAGACAGATGGAGCTTTTCAAGCAATAGAGACTATGAC 1107
 Db 64 TCCTTTCTGCTCGTGAAGTCTCTGACGAACTTTTCAAGCCATTAAGATTATGAT 123

Qy 1108 CCAGATGCAAGAGAGATGTTACACCACTTAAGAAGTTGATCATGACCTGTTTTT 1167
 Db 124 CCTGACAGTGAAGAAGCTTTTCACTTTTAAAAAGTTTACCATGATGATCCATTTTA 183
 Qy 1168 AATCCTGATCTCCTTGGAGAGACCACTATAAAAATGATTTTGCATATATGAGTCT 1227
 Db 184 AATCTTTAAACCTTTGGAGAAAGCCCTCTCAAGACATTTCTGATTTATGGGCTA 243
 Qy 1228 CATTTAAGAAGAGATTGGTTATTTACTTTGCCCAAGTGGCAAACTTATCTGATPAT 1287
 Db 244 GATTGGAAGCTGAGGTTGGTTACTTATTTTGACCAAGTGGGAAGCTTATCTGATPAT 303
 Qy 1288 TGGATCATCAGGATATCATTTAGCAAACTGAAGTTCCTCGTCAAGTCTGGAAT 1347
 Db 304 TGAATTTAAACAGATGATATATGAATGAAGATCTTGATTTCCGGTCAGAAAT 363
 Qy 1348 GTGATGATGGAAACGCTGACCTATTAAGTGGGATGAGACGATACCTATCATTCATC 1407
 Db 364 CTGATTAAAGAAACCTTGCTGCAACAGTGGGATGAGACGATACCATTCCTC 423
 Qy 1408 TCTTGTGCAAGAAATTGGCTCGGACCTTAAAGTTAACTAATGCTCCCAAGCAAG 1467
 Db 424 TCCTGTGCAAGAAATTGGCTGGGACCAAAAGTGAACATTAACAGACACAGCTCAGAG 483
 Qy 1468 CACGATGGAAGCAGCTCATGTGGAACCTAAATGATCATGACATGGCTCAGACATC 1527
 Db 484 CATGATGCTCAGCTGTACAGATGCATCAAAATATAGCATCAACATGTGGAGATATC 543
 Qy 1528 ATAGCTAATGACCAAAAGCAACCAAGGGTTAAGTACATTAACCTTTTGAAGACTTGAG 1587
 Db 544 ATCCCAATATGACAAAGTTAGTACATGAATGAGATACATTAACCTTTTATGAGATTCGAA 603
 Qy 1588 AGCATTCGGGGGAGAGAACCGCACTGTGGAGCTTGATTA 1629
 Db 604 AGTTTCCAGGAACGAGAACAGCAGTTGGAGCTTGATTA 645
 RESULT 8
 LOCUS BQ600021 792 bp mRNA linear EST 07-MAR-2003
 DEFINITION EST504916 cSTS Solanum tuberosum cDNA clone cSTS27C13 5' sequence, mRNA sequence.
 ACCESSION BQ600021
 VERSION BQ600021.1 GI:13617157
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 792)
 van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chien, A., Bougri, O., Buell, C.R., Roming, C., Tanksley, S. and Baker, B.
 Generations of ESTs from sprouting potato eyes Unpublished (2000)
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
 http://genome.arizona.edu/orders/
 Seq primer: M13F-R.
 Location/Qualifiers
 1..792
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="cSTS27C13"
 /tissue_type="sprouting eyes from tubers"
 /dev_stage="12-14 weeks post harvest"
 /lab_host="SOLR"

Db 421 GTTGACCTTGCGCCCTTCAAGTTCTGAGGAGACTGCTGCTTAATGTTCAATCTTTTG 480

Qy 803 CGTCGTCAATGTCGCTTATGCAATTTTCAAGAAATGGAAGGGTGTATAACAATCTCGGA 862

Db 481 GTTCATCAATGATGATGTTGCGATTTTCAAAATACTGTGAACAAGATATAGTACTGGA 540

Qy 863 CGCATTTTCTGGG 876

Db 541 AGCACTTTCTGAG 554

RESULT 10

CD10878 560 bp mRNA linear EST 25-JUN-2003

LOCUS VVA026C02.402285 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera

DEFINITION cDNA clone VVA026C02.5, mRNA sequence.

ACCESSION CD10878

VERSION CD10878.1 GI:32245059

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 560)

Cramer/G.R. and Cushman,J.C.

An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay unpublished (2002)

JOURNAL

COMMENT Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR PRIMERS

FORWARD: T3 20mer

BACKWARD: T7 21mer (backward)

Plate: 026 row: C column: 02

Seq primer: T7 20mer (forward)

High quality sequence stop: 560.

Location/Qualifiers

1..560

/organism="Vitis vinifera"

/mol_type="mRNA"

/db_xref="taxon:29760"

/clone="VVA026C02"

/tissue_type="leaf"

/dev_stage="juvenile and adult"

/clone_1lb="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Query Match 20.9%; Score 343; DB 6; Length 560;

Best Local Similarity 77.2%; Pred. No. 2.6e-91;

Matches 429; Conservative 0; Mismatches 126; Indels 1; Gaps 1;

Qy 1016 CCAGCATGGAATGTGGCCTTCCACCCCTTTGTCTTTCACAGCCCGTGAACATGAGATG 1075

Db 5 CTACATGTGATGTGATCTCCCACTCAGTTATCTTTCGCTGTAGATATCAGATG 64

Qy 1076 GGA-CTCTTTCAAGCAATAGAGACTATGACCCAGATAGCAAGAGATGTTACACCG 1134

Db 65 GAACNCCTTTTCAAGCAATAGAGGGTATGATTCAGATAGCAAGAGGCTCTTGACCA 124

Qy 1135 TTAAAGAGTGTATCATGATGACCCCTGTTTAAATCTCTGACTCTTCGAGAGACCA 1194

Db 125 TTACAGAGTTATATCATGGTATCGAGTTTGATATCACTTACCATGGAGACCA 184

Qy 1195 CCTATAAAAATGATTTTTCATATATGTCCTCATCTAAAGACAGAGTTGTTATAC 1254

Db 185 CCTTTAAGAAACATTTTGTATCTATGGAATAAATTAAGACTGAGTTGGTTATAT 244

Qy 1255 TTGGCCCAAGTGGCAACCTTATCTGATATATGATTCATACGATATCATTTAGCA 1314

Db 245 TTTCACCAAGTGGAAAGCCGTATCTGATATACGATATCATGACTGATCATTTATGAG 304

Qy 1315 ACTGAAGTTCCTCGTCAAGGCTGGAAGTGTGTTAGTGGAAAGCTGACCTATA 1374

Db 305 ATTGAAGATCTTAACTCAAGTCAAGAAATCTAGTGAAGGAAACCAAGAGCTGCC 364

Qy 1375 ACTGGGATGAGACGATACCTTATCATCTCTCTTGTCGCAAGAAATGGCTCGACCT 1434

Db 365 AGTGGGATGAGACGATTCATATCATCTCTCTTGTCGCAAGAAATGGCTTGCGCA 424

Qy 1435 AAGTTAATACATACATGCTCCCGACCCAGAACATGAGACGATCATGTGGA 1494

Db 425 AAGTGAACATACAAAGAGCTCCAGTGGAGCATGATGATCTGACATCAAGTGGAG 484

Qy 1495 CTAAATGTTATCATGAGCATGGGTGACATCATAGTAAACATGACAAAGCAAG 1554

Db 485 TTCAATGTAGAACATCATCTGATGAAATATATAGTCCCATATGACAGAGTCACTCGG 544

Qy 1555 GTTAAGTACATTAACCT 1570

Db 545 GTTAAGTATATTAACCT 560

RESULT 11

CA090564 676 bp mRNA linear EST 23-SEP-2003

LOCUS SCSGAM2105C04.5 AM2 Saccharum officinarum cDNA clone SCSGAM2105C04

DEFINITION 5', mRNA sequence.

ACCESSION CA090564

VERSION CA090564.1 GI:34943871

KEYWORDS EST.

SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 676)

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

The libraries that made SUCSEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

CONTACT: Arruda P

Centro de Biologia Molecular e Engenharia Genética

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>

plate: 105 row: C column: 04

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1..676

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCSGAM2105C04"

/lab_host="DH10B"

/clone_1lb="AM2"

/note="Organ: Apical meristem and tissues surrounding of immature plants; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from

[Apical meristem and tissues surrounding of immature plants]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucsec1.lad.ic.unica.br/public>

ORIGIN

Query Match 20.2%; Score 331.8; DB 6; Length 676;
Best Local Similarity 75.5%; Pred. No. 6,6e-88;
Matches 425; Conservative 0; Mismatches 137; Indels 1; Gaps 1;

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QY 79 GCGGAGGAGTGAACGAGTTTACGCGGCTGAGAGCTATGCGGTATATCTT 138
DB 114 GCGGCGGGGCGGAGCGGCGCGGAGTTTCCAGATTCGCGGAGTATCATTC 173
QY 139 CCGGAGTTTGGCTGACGACGACGACGAGCTGATCTTGAATGATACACTCCG 198
DB 174 CCGGGGTTCCGCTCAGCGCAGCTGCGCGGTGCTGCTGATGCGCCCTACCGCC 233
QY 199 TTGACATTCATCCGCTGACCTGATGCTGACACCACTAACCTTCTTGCTGTC 258
DB 234 TTGACATTCATCCGCTGACCTGATGCTGACACCACTAACCTTCTTGCTGTC 293
QY 259 AACTGCTGCTTAAAGTATGATGCTGATGCTGATGCTGATGCTGATGCTGATG 318
DB 294 AATGCTGCTTAAAGTATGATGCTGATGCTGATGCTGATGCTGATGCTGATG 353
QY 319 AAGTACGCGCTGACAGTGTCTTTCACGCACTACAGATTCAGAGTTACATACA 378
DB 354 AAGTACGCGCTGACAGTGTCTTTCACGCACTACAGATTCAGAGTTACATACA 413
QY 379 GGTCTCTTTTCTACTGCTGAGAAAGTGGCTTAAAGTGTGTTGATGTTAGAA 438
DB 414 GGTCTCTTTTCTACTGCTGAGAAAGTGGCTTAAAGTGTGTTGATGTTAGAA 473
QY 439 GCAATGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 498
DB 474 GCTATGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
QY 499 CGTACCTTTACTTTCACAGCTCAAGTGAACCTTTGAACTGCTTAAACT-CCGTGG 557
DB 534 CGAATCTGTTTTCACAAATTAAGTTTACTTTGAACTGCTTAAACTCCCGGG 593
QY 558 CGGCTCTTCTAATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 617
DB 594 AGGGCATCTTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
QY 618 ATGCTGAGCTAGAAATTCAC 640
DB 654 ATGCTGAGCTAGAAATTCAC 676

```

RESULT 12

LOCUS A1974291 534 bp mRNA linear EST 26-AUG-1999
DEFINITION T110293e KVO Medicago truncatula cDNA clone, pKV0-1E14, mRNA

ACCESSION A1974291
VERSION A1974291.1 GI:5776732

KEYWORDS EST

SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosoids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.

REFERENCE 1 (bases 1 to 534)

AUTHORS Vandenbosch,K., Hur,J., Moore,J., Beremand,P., Peng,H. and Ellis,L.
TITLE ESTs from uninoculated roots of Medicago truncatula (1999b)
JOURNAL Unpublished (1999)

COMMENT

Contact: Vandenbosch K
Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenbosch@umn.edu
Other name: 07-B-7; date: 6/30/99; Submitted to the Database of
Expressed Sequence Tags (dbEST) on 08/25/99; More information is
available at <http://chryste.tamu.edu/medicago>.
Seq primer: SKmod (CTA GAA CTA GTG GAT CC).
Location/Qualifiers
1..534

FEATURES

source

/organism="Medicago truncatula"
/mol_type="mRNA"
/culivar="genotype A17"
/db_xref="taxon:380"
/clone="pKV0-1E14"
/tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
/lab_host="E. coli strain XL0R"
/clone_lib="KV0"
/note="Vector: pluescript SK -; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-aseIst
helper phage and propagated in XL0R cells."

ORIGIN

Query Match 19.3%; Score 316.4; DB 1; Length 534;
Best Local Similarity 76.3%; Pred. No. 2,6e-83;
Matches 389; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

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DB 25 TTTCAGAAATCCCGAGGCCAATTTGCCGATGATGATGATGATGATGATGAT 84
QY 1049 CTTTCACAGCCCGTGAATCAGATGAGACTCTTTTCAGAGCAATAGAAATCTATGACC 1108
DB 85 CTTTCTCAGCTCGTGAATAGCGGATGCTCTTTTCAGAGCAATAGAAATCTATGACC 1144
QY 1109 CAGATGAGAGAGATGTTACACAGTTTAAAGATGTATTCATGATGAGACCTGTTTTTA 1168
DB 145 CAGACAGCAAGAGACTCTTGTACCAATTAAGAAATCATATCTTGATCTGTTACTTA 204
QY 1169 ATCTCTGACTCTTTGGAGAGACCACTATTAATAATGATTTTGCATATATGCTGCTC 1228
DB 205 ATCCACTTACACTTTGGGATGCGCCACCAATTAATAATGATTTTGCATATATGCGAGTA 264
QY 1229 ATCTTAAGACAGAGTGTGTTATTAATCTTTGCCCCAAGTGGCAACCTTATCTGTAATTT 1288
DB 265 ATTCAGAAACAGAAAGTGTGTTATTAATCTTTGCCCCAAGTGGCAACCTTATCTGTAATTT 1324
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DB 325 GGATCATCAGGATATATTAAGAACTGAAGGTTCTTATGATCAAGAGTCTGGAATTC 384
QY 1349 TGGTTGATGAGAGCTGAGACTTAACTGGGATGAGACGGTACCTTATCAATTCATCTCT 1408
DB 385 TGGTTGATGAGAGACCTGAGACTTAAAGTGGCGATGAGACGGTTCATTAACAACCTCCAT 444
QY 1409 CTTGGTGCAGAAATTTGGCTCGAGACTTAAAGTTAATCAATCAATGCTGCCAGCAGAAC 1468
DB 445 CTTGGTGCAGAAATTTGGCTCGAGACCAAGGTAACATTAACAGAGCTCTTCAGTCAGAAC 504
QY 1469 ACGATGAGAGGAGTACATGTGGAACCTA 1498
DB 505 ACGATGCTCAGATGTACAGATTTGATTTGA 534

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RESULT 13
BI267124          628 bp  mRNA  linear  EST 18-JUL-2001
LOCUS             NF097C071NF1054 Insect herbivory Medicago truncatula cDNA clone
DEFINITION        NF097C071N 5', mRNA sequence.
ACCESSION         BI267124
VERSION           BI267124.1
KEYWORDS          EST.
SOURCE            Medicago truncatula (barrel medic)
ORGANISM          Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; euroside 1; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.
1 (bases 1 to 628)
Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula insect herbivory library
Unpublished (2000)
JOURNAL
COMMENT           Contact: Korth K
                   Dept. of Plant Pathology
                   University of Arkansas
                   217 Plant Science Building, Fayetteville, AR 72701, USA
                   Tel: 501 575 5191
                   Fax: 501 575 7601
                   Email: khorth@comp.uark.edu
                   Insert length: 628 Std Error: 0.00
                   Plate: 097 row: C column: 07
                   Seq primer: TCACACAGAAACGCTATGAC.
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                   /clone="NF097C071N"
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                   /dev_stage="mature"
                   /clone_lib="insect herbivory"
                   /note="Vector: Lambda zap; Library was produced from fully
                   expanded M. truncatula leaves of plants fed upon by
                   Spodoptera exigua (beet armyworm) for 24 hours. Systemic
                   (undamaged leaves from injured plants) and wounded leaves
                   were harvested and pooled."
ORIGIN
Query Match      18.7%; Score 306.6; DB 4; Length 628;
Best Local Similarity 79.2%; Pred. No. 2.5e-80;
Matches 374; Conservative 0; Mismatches 97; Indels 1; Gaps 1;
QY 108 CGACTACTCGAAGCTATCGGGTATATCATTCGCGGATTTGGCTGACGACTACGAGC 167
DB 149 CGATTACTCTAAACTCTCGGCGATATATCCAGGCTTCGCTTACTACTCGACTTCGAGC 208
QY 168 GTGGTCATCTTGAAGTCTGCTCATATACCTCCGTGGACTTCATCCGCTGACCTCGATG 227
DB 209 ATGGCTATTTCTGACTGCCCTTACTCTCCGTAATTTCAATCTTCGATTTGGTTTG 268
QY 228 GCTAGACACCACTAAGTCTTTCTTGTGCTGTCNAAGTGGTTAAGTGATGGTCTTGA 287
DB 269 GCTGCACACCACTAAGTCTTTCTTGTGCTGTCNAAGTGGTTAAGTGATGGTCTTGA 328
QY 288 TCCCTTATATCAACACAGACCATCCGAGTGAAGTACAGGCGCTGACAGTGGTCTTTCAGC 347
DB 329 CCGCTTATCAATCAACACAGATCATCTGATTTGATATCCGCTCGATACCGGCTCTTCCGG 388
QY 348 CATCAAGAAATTTGATCCAGGTTATATTAACAGAGTCTCTTTCTACTGCTCTGAAAAGAGT 407
DB 389 AATTACAGAGCTGTGATCCAGGTTATATTAACAGAGCTCTTTCGCTGTATGAGAAAGATG 448
QY 408 GCTTAAGTGGTGTGTTAGTTGTTATGAAGCAATGCAATTTGCGCTGTTCCATAGA 467
DB 449 GATTAGTGTGTATTTGATTTGGCATTAAGAAGCTATATGCAATTAATGCTGTTCTTATGA 508

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QY 468 TTGAGATTTGTACCAACCAATTTGAAGAGCGTGACCTTTACTTTCAACAGCTCAAGTT 527
DB 509 TTGAGAGCTGTACCAATTCATGCTTTGAAGAAGACAGACTTTACTTATTAAGCTTAATTT 568
QY 528 GACCTTTGAAACGCTTTAAACCTCGCGGCGCTTCATATGATTTGGC 579
DB 569 GACATTTGAGACTGCTTT-CAACTTGAGAGGCGCCCTTTAATTTTGGC 619
RESULT 14
AU306500          728 bp  mRNA  linear  EST 22-JAN-2004
LOCUS             AU306500
DEFINITION        AU306500 zinnia cultured mesophyll cell equalized cDNA Zinnia
elegans cDNA clone Z16086, mRNA sequence.
ACCESSION         AU306500
VERSION           AU306500.1
KEYWORDS          EST.
SOURCE            Zinnia elegans
ORGANISM          Zinnia elegans
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Zinnia.
1 (bases 1 to 728)
Demura, T., Tashiro, G., Horiguchi, G., Kishimoto, N., Kubo, M.,
Matsuo, N., Minami, A., Nagata-Hiwataashi, M., Nakamura, K.,
Okamura, Y., Sasea, N., Suzuki, S., Yazaki, J., Kikuchi, S. and
Fukuda, H.
Visualization by comprehensive microarray analysis of gene
expression programs during transdifferentiation of mesophyll cells
into xylem cells
Proc. Natl. Acad. Sci. U.S.A. 99 (24), 15794-15799 (2002)
JOURNAL
COMMENT           Contact: Taku Demura
                   Morphogenesis Research Group
                   RIKEN Plant Science Center
                   1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan
                   Tel: 81-45-503-9605
                   Fax: 81-45-503-9573
                   Email: demura@postman.riken.go.jp
                   This clone was obtained at our laboratory
                   Seq primer: M13 forward.
FEATURES
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Query Match      17.9%; Score 293.4; DB 1; Length 728;
Best Local Similarity 70.3%; Pred. No. 2.5e-76;
Matches 484; Conservative 0; Mismatches 182; Indels 22; Gaps 6;
QY 442 AATGCAATTTGGCGGTG-TGCATACGATTTGGAGATTCACCAACCAATTTGAAGAGCG 500
DB 1 AATGCTATTTCTGCTGTGAGCATATGATGAGAGCTGACACATCGAAACTTGAAGAGCG 60
QY 501 TGACCTTTACTTTCAACAGCTCAAGTTGACCTTTGAAAGCTTTTAAACTCCGTGGCGG 560
DB 61 GGATTTGATCTTCCACAGAGCTCAACATTAATTTGAAAGAGCTTTAAACATCGTGGTGG 120
QY 561 CCTTTATATGATTTATCCCATTCATGAGGTATATATGCTTCAATATTCTT-TCGGAAT 619
DB 121 TCCATCATCGTATTTTCCCATCTCTCGGTAAACAAATTTTGGTATCTTTTATAGAGT 180
QY 620 GCGTGAAGCTTGAATTTGACCAACCAATTAATTTGAAGTGGCTGATCAGATATTCATG 679

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Db      181 GGTGAAGCTAGAAATTTCTCCAAAAGATATATCAATGCTAGATGATATACAGC 240
Qy      680 CTTATTTGGCTGGAGCTCCTCTTGGTTGTTGAGCAATCAATCTACTCT 739
Db      241 CTTACTTGTGTTGGAGCTCCTCTTGTGGTTCTGTCAGACAGTAGAGCAACACTCT 300
Qy      740 CTGGTGTAAAGCTTTGGCCTCTCTTCTTGAGAGAACTGCTGGTTGTTGTCATTTCTT 799
Db      301 CTGGTTCCACTTTTGGTTCTTCTCTATACCCGAGGGAGCGGCCGGTGTATGTTCAATTCAT 360
Qy      800 TTGCGTCTCATTTGGCTTATGCCATTTTCAAGATTGCAAGGGGTATTAACACATCTCT 859
Db      361 TCGGCTCTTCACTATGATGTACACTTTTCAAGATATTGACGATGATAAAACGTTCTACT 420
Qy      860 GGAGGCAATTTTCTGGGGGCTGCTGCAAGAAAGATGCGGTATACCACTGTAGTAGAG 919
Db      421 CAAGCAATTTTCTGGTGGGCGCAGAAAAACACA--TGTATATCATGTTGATGATC 477
Qy      920 AGGAATATCAATCAAAATATTTCTGGCTGGCGCAGCAAAATATTTAACTTGAATTC--- 976
Db      478 TTGAATATCGGTTAAACTATTTCTGGAATTTCCAACTAATATCAATTTGAGATCCCGT 537
Qy      977 -----CTTCCACTAGCGTTACAGAAACAGCTTCTAGTCAACTGACAGCATGG 1024
Db      538 CAGTATTTGAAGCTTATCATCTTTGGAGATGAATGACAGGCCAATTTATCTAATCAGTG 597
Qy      1025 AATGTGGCTTCCAC--CCTTTGTCTTCAAGCGCGTGAATAGAGAT--GGGACTCT 1082
Db      598 AATGTGGGCTCCCACTAATTTATCTTTCTGCTGTAATATGACAGATGGGACTTT 657
Qy      1083 TTTCAAGCAATAGAACTATGACCCA 1110
Db      658 TTTTAAAGCATGAGATATGATCTA 685

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RESULT 15
LOCUS   CA221313
DEFINITION SCGF4034D01.g FL4 Saccharum officinarum CDNA clone SCGF4034D01
5', mRNA sequence.
ACCESSION CA221313
VERSION   CA221313.1 GI:35275497
KEYWORDS  EST.
SOURCE    Saccharum officinarum
ORGANISM  Saccharum officinarum
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoidae; Andropogoneae; Saccharum; Saccharum officinarum
          complex.
REFERENCE 1 (bases 1 to 683)
AUTHORS  Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE     The libraries that made SUCEST
JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT   Contact: Arruda P
          Centro de Biologia Molecular e Engenharia Genetica
          Universidade Estadual de Campinas
          Caixa Postal 6010, 13083-970, Campinas SP, Brazil
          Tel: 55 19 3788 1137
          Fax: 55 19 3788 1089
          Email: parud@unicamp.br
          Clone distribution: clone distribution information can be found
          through the Brazilian clone collection Center (BCCC) at
          http://www.bcccenter.fcav.unesp.br
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FEATURES

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/note="Organ: Developed inflorescence and rachis (20cm-long); Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from (Developed inflorescence and rachis (20cm-long)). cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.iad.unicamp.br/public>"

ORIGIN

Query Match 17.8%; Score 291.8; DB 6; Length 683;
Best Local Similarity 66.6%; Pred. No. 7.3e-76;
Matches 457; Conservative 0; Mismatches 205; Indels 24; Gaps 2;

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Qy      552 CCGTGGCGGCCCTTCTATAGTATTTGCCCATTAATGGGTATATATGTTCAATCTT 611
Db      1 CCGAGGAGGGCCATCTTGGTATTTGCTCATTCGATGGAAATATATGTTTCCCTACTT 60
Qy      612 TCTGGAATGCTGAGGCTAGAAATTGSCAACAAACATTTATTTGAAGTGGCTTATCGCA 671
Db      61 TTTGGAATGTTGAAGCTGAAATTTGCTCCAGCACTATATCCAGTGGCTTGAAGACA 120
Qy      672 TATCCATGCTTATTTGCTGTTGAGCTCTCTTCTTGTGTTGAGGCAATCAATC 731
Db      121 TATACATGATACCTTTGCAAGTGGCGCTCTCTTGTGATCTATGACAGATTAGAG 180
Qy      732 TACTCTCTGTGTTAAAGTTGGCTCTCTCTGTTTCTGAGGAACCTGCTGGTTGTC 791
Db      181 TGCTCTTCTGGAACAACCTTTTGGTCTTCCAGTCAAGTAGAGGACAGACATGATGAT 240
Qy      792 CAATCTTTTGGCGTGCATTTGTTGCTTATGCTTATGCTTATGCTTATGCTTATGCT 851
Db      241 TAAATGCAATTTGCTCTCTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 300
Qy      852 CACATCTGAGCAGATTTTCTGGGGTGTGCTCAAGAAAGATTAAGCGCTATACCACTG 911
Db      301 TATCTACTGAAAGATTTTGTGAGGAAAGGA---GTTGTCTCTACAGACAACAATG 357
Qy      912 TGATGAAGAGATATATCAATCAAAATATTTGCTGTCGCGCAAAATATTTAACTTGA 971
Db      358 TGATGAAGCTGAATATATATATGACTAGCGCGAGATGGCCCAAGACCTTGTATATGGA 417
Qy      972 AATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACTGA----- 1015
Db      418 GGTTCCTTCAGTTGAGATATAGGGGGCATACCATCATCAGATATTAACCGAATCAT 477
Qy      1016 -----CCAGCATGGAATGTGGCTTCCACCCCTTTGCTTTCACAGCCCGTGAATAGC 1070
Db      478 AATCATCGATATGAGATGGCGGAAAGCCAACTCTCTGTCTATNTTCTGCGAGAAAGTGC 537
Qy      1071 AGATGGACCTCTTTTCAAGCAATAGAAAGACTATGACCCAGATAGCAAGAGATGTACA 1130
Db      538 AGATGTACTTTGTTTCAAGCAATAGAGATTAAGCCCTCAGAGCAAGGACCTTGTTA 597
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Qy      1191 ACCACCTATAAATAATGATTTTGA 1216
Db      658 AACCCCAATAAAGACATATTTGGCA 683

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 22:40:26 ; Search time 7037 Seconds
(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba: *
2: gb_hcg: *
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4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_scs: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1641	100.0	1641	6	AX090311 Sequence
2	911.8	55.6	2609	8	AF493159 Medicago
3	271.8	16.6	3896	6	BD271623 Novel cia
4	271.8	16.6	3896	6	BD271623 Novel cia
5	271.8	16.6	3896	6	AX037587 Sequence
6	271.8	16.6	3896	6	AX037606 Sequence
7	271.8	16.6	119914	8	AC003027 Arabidops
8	176.2	10.7	328	6	AX090328 Sequence
9	118	7.2	93398	8	AP006356 Lotus cor
10	113.4	6.9	118192	8	AP004120 Oryza sat
11	113.4	6.9	147123	8	AP005691 Oryza sat
12	113.4	6.9	158971	2	AP004882 Oryza sat
13	110.4	6.7	709	6	BD271624 Novel cia
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16	110.4	6.7	709	6	AX037607 Sequence
17	109	6.6	356	6	AX090329 Sequence
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28	49.4	3.0	1986	6	AX037595	Sequence	
29	49.4	3.0	1986	6	AX037597	Sequence	
30	49.4	3.0	1986	6	AX090382	Sequence	
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32	49.4	3.0	2575	8	SCYNR008W	Z71623 S.cerevisia	
33	49.4	3.0	23901	8	SCN201952	X71395 S.cerevisia	
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39	47.4	2.9	42391	8	SPBC776	AL035263 S.pombe c	
40	47.2	2.9	5907	10	RATCPE01	L07273 Rattus norv	
c	41	47.2	2.9	261278	2	AC107586	Rattus no
c	42	43.4	2.6	110000	8	CR380955_05	Continuation (6 of
c	43	43.4	2.6	300029	8	AB016899	Eremothec
c	44	42.8	2.6	1737	8	AY259955	Argyroxip
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ALIGNMENTS

RESULT 1	AX090311	1641 bp	DNA	linear	PAT 21-MAR-2001
LOCUS	AX090311	Sequence 4 from Patent WO016308.			
DEFINITION	AX090311.1	GI:13444180			
ACCESSION	AX090311.1	GI:13444180			
VERSION	AX090311.1	GI:13444180			
KEYWORDS					
SOURCE					
ORGANISM	Arabidopsis thaliana (chale cress)				
	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	rosids; eurooids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	1	Laessle, M. and van Bennaam, A.			
AUTHORS		Plant sterol acyltransferases			
TITLE		Patent: WO 0116308-A 4 08-MAR-2001;			
JOURNAL		MONSANTO COMPANY (US)			
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QY	61	ATTTCGGTGGCCGCAATCGCGTGAAGATGAGACCGGCTTACCGGAGCTACACGAG	120		
DB	61	ATTTCGGTGGCCGCAATCGCGTGAAGATGAGACCGGCTTACCGGAGCTACACGAG	120		
QY	121	CTATCGGATATATCATTCGCGGATTTTCGTCGACGACGCTACGAGCGTGTGATCTT	180		
DB	121	CTATCGGATATATCATTCGCGGATTTTCGTCGACGACGCTACGAGCGTGTGATCTT	180		
QY	181	GACTGTCCATACCTCCGCTGCACTTCATCGCTCGACCTCGTATGCGCTACACCACT	240		
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Qy 361 GATCCAGGTACATATAACAGTCTCTTCTAATGTCTGGAAGAGTGGCTTAAGTGT 420
Db 361 GATCCAGGTACATATAACAGTCTCTTCTAATGTCTGGAAGAGTGGCTTAAGTGT 420
Qy 421 GTTGATTTGGTAAAGCAAAATGCTGCTGTTCCATACGATTTGAGATTTGCA 480
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Qy 481 CCAACCAATTTGGAGAGCGTGAACCTTTAATTTCAAGCTCAAGTTGACCTTTGAA 540
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Qy 541 GCTTTAAATCTCCGTGGGCGCCCTTCTATAGTATTTGGCCATTCAGTGGTAAATGTC 600
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Qy 601 TTGAGATATCTTTCTGGAATGGCTGAGGCTAGAAATTCAGCAAAACATTTATTTGAAGTGG 660
Db 601 TTGAGATATCTTTCTGGAATGGCTGAGGCTAGAAATTCAGCAAAACATTTATTTGAAGTGG 660
Qy 661 CTGATCAGCATATCCATGCTTATTTCCGTGTGAGAGTCCCTCTTCTGTTGTTCTGTAG 720
Db 661 CTGATCAGCATATCCATGCTTATTTCCGTGTGAGAGTCCCTCTTCTGTTGTTCTGTAG 720
Qy 721 GCAATCAATCTACTCTCTGCTGTAAAGTGGCTTCCCTGTTCTGAGGAACTGCT 780
Db 721 GCAATCAATCTACTCTCTGCTGTAAAGTGGCTTCCCTGTTCTGAGGAACTGCT 780
Qy 781 CGGTGTTGTCGAATCTTTTGGCGTCAATGTGGCTTAATGCAATTTTCAAGAAATGTC 840
Db 781 CGGTGTTGTCGAATCTTTTGGCGTCAATGTGGCTTAATGCAATTTTCAAGAAATGTC 840
Qy 841 AAGGCTGATTAACATCTCTGAGCGAATTTTCTGGGGGTGCTGCAAAAGAAATAGGCG 900
Db 841 AAGGCTGATTAACATCTCTGAGCGAATTTTCTGGGGGTGCTGCAAAAGAAATAGGCG 900
Qy 901 GTAATCAGCTGATGAGAGAGATATCAATCAAAATATTTGCTGGCCGCAAAATAT 960
Db 901 GTAATCAGCTGATGAGAGAGATATCAATCAAAATATTTGCTGGCCGCAAAATAT 960
Qy 961 ATTAACATTTGAATCTCTTCCACATGAGGTTACAGAAACAGCTTATGCAACATGACNAGC 1020
Db 961 ATTAACATTTGAATCTCTTCCACATGAGGTTACAGAAACAGCTTATGCAACATGACNAGC 1020
Qy 1021 ATGGAATGGGCTTCCACCTTTTGTCTTCAAGCCCGTGAACCTAGCAGATGGGACT 1080
Db 1021 ATGGAATGGGCTTCCACCTTTTGTCTTCAAGCCCGTGAACCTAGCAGATGGGACT 1080
Qy 1081 CTTTCAAGCAATAGAGACTATGACCAAGATGACAGAGAGATGTTACACAGTTAAAG 1140
Db 1081 CTTTCAAGCAATAGAGACTATGACCAAGATGACAGAGAGATGTTACACAGTTAAAG 1140
Qy 1141 AAGTGTATCATGATGACCTGTGTTTAACTCTGACTCTTGGAGAGACCACTATA 1200
Db 1141 AAGTGTATCATGATGACCTGTGTTTAACTCTGACTCTTGGAGAGACCACTATA 1200
Qy 1201 AAAATGTATTTTGGATATATGCTCATCTTAAAGACAGAGTGTATTTACTTTGCC 1260
Db 1201 AAAATGTATTTTGGATATATGCTCATCTTAAAGACAGAGTGTATTTACTTTGCC 1260
Qy 1261 CCAAGTGGCAAACTTATCTGATATTTGATCATCAGGATATCATTTTACGAACCTGAA 1320
Db 1261 CCAAGTGGCAAACTTATCTGATATTTGATCATCAGGATATCATTTTACGAACCTGAA 1320

Qy 1321 GGTTCCTGCTGTCAAGGCTTGAACCTGTGTGATGGAACGCTGACCTTAACTGGC 1380
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Qy 1381 GATGAGACGGTAAACCTTATCATTTCACTCTCTTGTGTGCAAGAAATTTGGCTGGAAGTT 1440
Db 1381 GATGAGACGGTAAACCTTATCATTTCACTCTCTTGTGTGCAAGAAATTTGGCTGGAAGTT 1440
Qy 1441 AACATAACATGAGTCTCCAGCAGAACAGATGGAAGCGATCATGTGGAACCTAAAT 1500
Db 1441 AACATAACATGAGTCTCCAGCAGAACAGATGGAAGCGATCATGTGGAACCTAAAT 1500
Qy 1501 GTTGATCATGAGCATGGGTGAGACATCATACTATGACAAAAGCAGCAAGGTTAAG 1560
Db 1501 GTTGATCATGAGCATGGGTGAGACATCATACTATGACAAAAGCAGCAAGGTTAAG 1560
Qy 1561 TACATTAACCTTTTATGAAAGATCTGAGAGCATTCGCGGGAAGAGAACCGAGTGGAG 1620
Db 1561 TACATTAACCTTTTATGAAAGATCTGAGAGCATTCGCGGGAAGAGAACCGAGTGGAG 1620
Qy 1621 CTGATTAAGTGGGTATTTAA 1641
Db 1621 CTGATTAAGTGGGTATTTAA 1641

RESULT 2
AF493159
LOCUS
DEFINITION
Medicago truncatula putative phosphatidylcholine acyltransferase
mRNA, complete cds.
ACCESSION
AF493159
VERSION
AF493159.1 GI:25992000
KEYWORDS
Medicago truncatula (barrel medic)
SOURCE
ORGANISM
Medicago truncatula
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE
1 (bases 1 to 2609)
Benveniste, P., Bouvier-Nave, P., Schaller, H. and Noiriel, A.
Acyltransferases involved in lipid (sterol) biosynthesis
JOURNAL
TITLE
Unpublished
AUTHORS
Benveniste, P., Bouvier-Nave, P., Schaller, H. and Noiriel, A.
REFERENCE
2 (bases 1 to 2609)
Direct Submission
Submitted (15-MAR-2002) Plant Molecular Biology Institute, CNRS, 28 rue Goethe, Strasbourg 67083, France
JOURNAL
TITLE
Unpublished
FEATURES
source
1..2609
Location/Qualifiers
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone_lib="Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library (Korth, K., et al., unpublished)"
/note="fabaceae; sequence derived from EST clones BE31377 and B1267156"
82..1980
/note="enzyme involved in the metabolism of phospholipids and sterols"
/codon_start=1
/product="putative phosphatidylcholine acyltransferase"
/protein_id="AA077002.1"
/db_xref="GI:25992001"
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ORIGIN

PMQDRPLKNIKFCITGNSKTKKVCYIYFABGKRPDMWITTDVVEYBESLYTRAGNLY
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VFNNTIRPVRKYITYEYEDSLGKGTATWELDKAHHRIYASSLYMRELYLMMWRDII
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ADLLHTLT"

Query Match	55.6%	Score 911.8;	DB 8;	Length 2609;
Best Local Similarity	75.6%	Pred. No. 1,8e-253;		
Matches 1167; Conservative	0;	Mismatches 352;	Indels 24;	Gaps 2;

Qy	108	CGACTACTCGAAGCATATGGGTATATATATATTCCTGGGATTTTCGTCGACGACGATCAACGAC	167
Db	168	CGATTACTCTAAACCTCCGGGACTATATATCCAGAGGCTTGCCTTCTACTCAGGCTCCGAGC	227
Qy	168	GTGTCGATCCTTGACTGTCCATACATCTCCGTTGGACTTCAATCCGCTGCACCTCGATG	227
Db	228	ATGGCTATTCCTTGACTGCCCCCTTACTCTCCGCTAGATTTCATCTCTCGATTGGCTTGG	287
Qy	228	GCTTAGACCACTAAGCTTCTTTCTGCGTGTCAACGTGCGTGGTTTAAGATGTATAGTGCTAGA	287
Db	288	GCTGACACCAACCAACTTCTTTCTGCTGTGAATTTGGCTTAAAGTTCATAGTGTGTGGGA	347
Qy	288	TCCTTATATCAAAACAGACCAATCCCGAGTGTAAAGTCAAGGCGCTGCACAGTGTCTTTCAGC	347
Db	348	CCCTTATCAATCAAAACAGATCATCTCGATTGTAAATCCCGCTGTGATAGCGGCTTTCGGG	407
Qy	348	CATCAACAGATTGGATCCAGGTTACATPAACAGTCTCTTCTTCTACTGTCTGTGAAAAGATG	407
Db	408	AATTACAAAGGCTTGATCCAGGTTATATPAACAGGACCTTCTTCGTGTATGTGAAAAGATG	467
Qy	408	GCTTAAGTGTGTGTGTGATTTGGTATGTGAAGCAAAATGTCGTGCTTTCATACGA	467
Db	468	GATTBAGTGTGTATTTGAATTTGGCATGTAACTATATGCAATATTTGCTGTCTTATGGA	527
Qy	468	TTGGAGATTGTCAACCAACCAAAATGGAAAGAGCGTACCTTTACTTTCACAAAGCTCAAGTT	527
Db	528	TTGGAGACTGTACACCATCATGTCTGAAAGAAAGAGACCTTTACTTTCATTAAGCTTAAATY	587
Qy	528	GACCTTTGAAACTGCTTTAAAATCCGTGGGCGGCGCTCTATAGTATTGGCCATTCAT	587
Db	588	GACATTGTGAGCTGCTTTCAAACTTCGAGGTGGCCCCCTTTAGTTTGTGCTATCACT	647
Qy	588	GGGTATATATGTCTTCAGATATCTTCTGGAATGCGTGAAGGCTAGAAATTGCAACAAACA	647
Db	648	GGGTATATACGTTTTTTCGTTATTTCTTGAAGTGTGAAGCTGAAGAAATTGCAACAAACA	707
Qy	648	TTATTTGAAGTGGCTTGATCAGCATATCAGTCTTATTTGCTGTGGAGCTCCTCTTCT	707
Db	708	TTATATCCAAATGGCTGATCAACAATATCATGCTTATTTTCTGTGCTGCCACTTCT	767
Qy	708	TGCTTCTGTGAAGCAATCAAAATCTACTCTCTGCTGTGAAGCTTGGCGCTTCCGTTTC	767
Db	768	GGGTGTCACTGAAMACATTTGAAGCAACCTTTCGGATTTCACTTTGTCTTCCAGTATC	827
Qy	768	TGAGGGAATCTGCTCGTGTGTGCCAAATCTTTTCCGTGCTCATTTGAGCTTATGSCACTT	827
Db	828	TGAGGGAACACTGCATGTGATGTTCACTCTTTGCTTCTGTCAATGTGTGAATGATGCTT	887
Qy	828	TTCAAGAATTGCAAGGCTGATPAACATCTCTGACGCAATTTTCTGGGGGTCTGCAA	887
Db	888	TTCCAAAGTACTGTAGAGCAAGTAAATAATTTGAAAGCAATTTTCTGAGGAAAGCAAGT	947
Qy	888	GAAAGATTAAGGGCGTATACCACTGTGATGAAGAAAGGAATATCAATAAATAATTCGGCTG	947
Db	948	---AGTATCCAAATACATATACCTGTGAAGAGGAGGATTAAGTCAAACTTTTCTGTGATG	1004
Qy	948	GCCGCAATAATTTATTAACATTTGAATTTCTTCCACTAGCG-----	988
Db	1005	GCCAAACAAGATTAATCAACATTGAATTTCTTCAACCGGTGGAATTTGAAGCATATCCCTC	1066
Qy	989	---TTACGAACAGCTCTATGTACATGACCAAGATGGAATGTGGCTTTCCACCTTTT	1046

Db	1065	ATTTTCAGAAATCCCCGAGGCCCACTGTCCGGAAATGGAATGTGGACTTCACTCACTT	1128
Oy	1047	GTCTTTCAACGCCCGTAAATCAGAGAGATGGGACCTTTTCAAACCAATPAGAAACTATTA	1106
Db	1125	ATCTTTCTCAGCTCGTGAATAATAGCGAGATGCGCTCTTTTCAAGCCAAATTGAAGATTATGA	1188
Oy	1107	CCGAGATTGCAAGAGAGATGTTACACCAAGTTAAAGAGTTGTATCATGATGACCCGTGTTT	1166
Db	1185	CCGAGACAGCAAGAGACTCTTGTACCAATTAGAAATCATATCTTGGTGAATCCGTACT	1244
Oy	1167	TAACTCTCTGACTCCTTGGGAGAGACCACTATTAATAATATATTTTGCATATATGTGTC	1222
Db	1245	TAAATCCATTACACTTTGGGATCCGCCACCAATAAAAACGTGTCTGCATTTATGCGAG	1304
Oy	1227	TCATCTAAAGCAGAGGTGGTATTTACTTTGCCCAAGTGGCAAACTTATCCGATATA	1286
Db	1305	TAAATTCAAAGCAAAAGTTGGTGTACTACTTTTGCCCTTAGCGGCAAGCCGTATCTGTATTA	1366
Oy	1287	TTGGATCATCAGGATATCATTTTACGAAACTGAAGGTTCCCTCGTTCMAAGSTGTGAAC	1348
Db	1365	CTGGATCATTTACAAATGTCTGTTTAGTATAGAAAGGATCTTAAGTCAACAAAGTCAGGAAA	1422
Oy	1347	TGTGTTGATGGGAACGCTGGAACCTATTAACCTGGGATGAGACGGTATCCCTATCATCACT	1406
Db	1425	TCTGTTGTAAGGGGAACCTGTGATCTATTAAGTGGGATGAGACGGTTCATTAACACTCCCT	1484
Oy	1407	CTCTTGGGCAAGAAATTTGGCTCGGACCTAAAGCTTAACATTAACAAATGGCTCCCAAGCCAGA	1466
Db	1485	ATCTTGGGCAAAATTTGGCTGGGACCAAAAGTGAACATTACAAGAGCTCTCTCAAGTCAGA	1544
Oy	1467	ACACGATGGAAGCAGACGTACATGTGGAACCTAAATGTTGATCATGACGATGGGTCAAGACAT	1528
Db	1545	ACACGATGTGTCAAATGTACAAATGTGAATTTGAATGTGGAACATCACTATGTGAAGATGATAT	1604
Oy	1527	CATAGCTAACATGACAAAAGCAACCAAGGTTTAAGTACATAAACCCTTTATGAAAGACTCTGA	1586
Db	1605	TGTTTCAAAACATGACAAAGTTCCTAGGGTTAAGTACATAACATATATATGAAAGATTCTGA	1664
Oy	1587	GAGCATTCGGGGGAAGAAACCGAGAGTCTGGAGCTTGATATAA 1629	
Db	1665	AAGTCTTCAGAAAGAGAGACACAGCTTTGGAGCTTGATATAA 1707	

RESULT 3	BD271623	3896 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD271623				
DEFINITION	Novel class enzyme in biosynthesis pathway of tricyclicglycerol production and recombinant DNA molecule encoding the enzyme.				
ACCESSION	BD271623.1	GI:33081391			
VERSION	JP 2002541783-A/8.				
KEYWORDS	Arabidopsis thaliana (thale cress)				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Arabidopsids				
	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroside II; Brassicales; Brassicaceae; Arabidopsids.				
REFERENCE	1 (bases 1 to 3896)				
AUTHORS	Dallwitz, A., Stahl, U., Lemann, M., Banas, A., Rome, H. and Stryme, S.				
TITLE	Novel class enzyme in biosynthesis pathway of tricyclicglycerol production and recombinant DNA molecule encoding the enzyme				
JOURNAL	Patent: JP 2002541783-A 8 10-DEC-2002;				
COMMENT	BASF PLANT SCIENCE GMBH				
	OS Arabidopsis thaliana (thale cress)				

of triacylglycerol
production
CC and recombinant DNA molecule encoding the enzyme FH Key
Location/Qualifiers
FT source 1..3896
/organism='Arabidopsis thaliana' (thale FT
cress)'.
Location/Qualifiers
1..3896
/mol_type='genomic DNA'
/db_xref='taxon:3702'

ORIGIN

Query Match 16.6%; Score 271.8; DB 6; Length 3896;
Best Local Similarity 80.0%; Pred. No. 2.7e-67;
Matches 375; Conservative 0; Mismatches 2; Indels 92; Gaps 1;

QY 768 TGAGGGAACGTCGCTGTTGTCCTCAATCTTTTGGCGTCATTTGCTTATGCCATT 827
DB 1787 TCAGGGAACGTCGCTGTTGTCCTCAATCTTTTGGCGTCATTTGCTTATGCCATT 1846

QY 828 TTCAGGAATTCGCAAGGCGTATACACATCTGTGATGAAGAGATATCAATCAATATTTCTGCGCTG 947
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QY 888 GAAAGATAGCGCGGTATACCACTGTGATGAAGAGATATCAATCAATATTTCTGCGCTG 947
DB 1907 GAAAGATAGCGCGGTATACCACTGTGATGAAGAGATATCAATCAATATTTCTGCGCTG 1966

QY 948 GCCGCAAAATATTTATTAACATTGAAATCTTCCACTAGC----- 987
DB 1967 GCCGCAAAATATTTATTAACATTGAAATCTTCCACTAGCCTGTATATGCA 2026

QY 988 ----- 987
DB 2027 ACTGTAACTATACAAAAGTTTCCACCAAGATGTTCACTCTCATATTTCCCTTTGAT 2086

QY 988 -----GTTACGAAACAGCTCTAGTCAACATGACCAAGATGATGCGCTT 1035
DB 2087 GTGTATCATCATGTTACAGAAACAGCTCTAGTCAACATGACCAAGATGATGCGCTT 2146

QY 1036 CCCACCTTTTGTCTTTTCAACAGCCCGTGAACCTAGAGATGGAGCTTTTCAAGCAATA 1095
DB 2147 CCCACCTTTTGTCTTTTCAACAGCCCGTGAACCTAGAGATGGAGCTTTTCAAGCAATA 2206

QY 1096 GAAAGCTATGACCCAGATAGCAAGAGATGTTACACAGTTAAAGAGT 1144
DB 2207 GAAAGCTATGACCCAGATAGCAAGAGATGTTACACAGTTAAAGAGT 2255

RESULT 4
BD271633 3896 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Novel class enzyme in biosynthesis pathway of triacylglycerol
production and recombinant DNA molecule encoding the enzyme.
ACCESSION BD271633
VERSION BD271633.1 GI:33081401
KEYWORDS JP 2002541783-A/18.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 3896)
Dahlgvist, A., Stahl, U., Lemman, M., Banas, A., Ronne, H. and Styenne, S.
Novel class enzyme in biosynthesis pathway of triacylglycerol
production and recombinant DNA molecule encoding the enzyme
Patent: JP 2002541783-A 18 10-DEC-2002;
JOURNAL BASF PLANT SCIENCE GMBH
COMMENT OS Arabidopsis thaliana (thale cress)
PN JP 2002541783-A/18
PD 10-DEC-2002

PF 28-MAR-2000 JP 2000609586
PR 01-APR-1999 EP 99106656.4, 10-JUN-1999 EP 99111321.8 PR
07-FEB-2000 US 60/180687
PI ANDERS DAHLQVIST, ULF STAHL, MARIT LENMAN, ANTONI BANAS PI
HANS RONNE, STEN STYME
PC C12N15/09, A01H5/00, C12N1/19, C12N5/10, C12N9/10, C12P7/64// PC
(C12P7/64, C12R1:645), (C12P7/64, C12R1:91), C12N15/00, C12N5/00 CC
Novel class enzyme in biosynthesis pathway
of triacylglycerol
production
CC and recombinant DNA molecule encoding the enzyme FH Key
Location/Qualifiers
FT source 1..3896
/organism='Arabidopsis thaliana' (thale FT
cress)'.
Location/Qualifiers
1..3896
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/mol_type='genomic DNA'
/db_xref='taxon:3702'

ORIGIN

Query Match 16.6%; Score 271.8; DB 6; Length 3896;
Best Local Similarity 80.0%; Pred. No. 2.7e-67;
Matches 375; Conservative 0; Mismatches 2; Indels 92; Gaps 1;

QY 768 TGAGGGAACGTCGCTGTTGTCCTCAATCTTTTGGCGTCATTTGCTTATGCCATT 827
DB 1787 TCAGGGAACGTCGCTGTTGTCCTCAATCTTTTGGCGTCATTTGCTTATGCCATT 1846

QY 828 TTCAGGAATTCGCAAGGCGTATACACATCTGTGATGAAGAGATATCAATCAATATTTCTGCGCTG 947
DB 1847 TTCAGGAATTCGCAAGGCGTATACACATCTGTGATGAAGAGATATCAATCAATATTTCTGCGCTG 1906

QY 888 GAAAGATAGCGCGGTATACCACTGTGATGAAGAGATATCAATCAATATTTCTGCGCTG 947
DB 1907 GAAAGATAGCGCGGTATACCACTGTGATGAAGAGATATCAATCAATATTTCTGCGCTG 1966

QY 948 GCCGCAAAATATTTATTAACATTGAAATCTTCCACTAGC----- 987
DB 1967 GCCGCAAAATATTTATTAACATTGAAATCTTCCACTAGCCTGTATATGCA 2026

QY 988 ----- 987
DB 2027 ACTGTAACTATACAAAAGTTTCCACCAAGATGTTCACTCTCATATTTCCCTTTGAT 2086

QY 988 -----GTTACGAAACAGCTCTAGTCAACATGACCAAGATGATGCGCTT 1035
DB 2087 GTGTATCATCATGTTACAGAAACAGCTCTAGTCAACATGACCAAGATGATGCGCTT 2146

QY 1036 CCCACCTTTTGTCTTTTCAACAGCCCGTGAACCTAGAGATGGAGCTTTTCAAGCAATA 1095
DB 2147 CCCACCTTTTGTCTTTTCAACAGCCCGTGAACCTAGAGATGGAGCTTTTCAAGCAATA 2206

QY 1096 GAAAGCTATGACCCAGATAGCAAGAGATGTTACACAGTTAAAGAGT 1144
DB 2207 GAAAGCTATGACCCAGATAGCAAGAGATGTTACACAGTTAAAGAGT 2255

RESULT 5
AX037587 3896 bp DNA linear PAT 16-NOV-2000
LOCUS
DEFINITION Sequence 11 from Patent WO0060095.
ACCESSION AX037587
VERSION AX037587.1 GI:11227006
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Banas, A., Stahl, U., Styenne, S., Lemman, M., Ronne, H. and Dahlqvist, A.

TITLE A new class of enzymes in the biosynthetic pathway for the production of triacylglycerol and recombinant dna molecules encoding these enzymes
JOURNAL Patent: WO 0060095-A 11 12-OCT-2000;
BASF PLANT SCIENCE GMBH (DE); BANAS ANTONI (PL); STAHL Ulf (SE); STYME STEN (SE); LENMAN MARI (SE); RONNE HANS (SE); DAHLQVIST ANDERS (SE)

FEATURES
source Location/Qualifiers
1..3896
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN

Query Match 16.6%; Score 271.8; DB 6; Length 3896;
Best Local Similarity 80.0%; Pred. No. 2.7e-67;
Matches 375; Conservative 0; Mismatches 2; Indels 92; Gaps 1;
768 TGAGGAACCTGCTCGGTGTTGTGTCGAATTCCTTTGCGTGCATTTGGCTTATGCCATT 827
1787 TCAGGGAACCTGCTCGGTGTTGTGTCGAATTCCTTTGCGTGCATTTGGCTTATGCCATT 1846
QY 828 TTCAAAGATTGCAAGGGTGATACACATCTCGACGCAATTTTCTGGGGGTGCTGCAA 887
DB 1847 TTCAAAGATTGCAAGGGTGATACACATCTCGACGCAATTTTCTGGGGGTGCTGCAA 1906
QY 888 GAAAGATAGGCGGTATACACTGTGATGAAGAGAAATATCAATAATATTCGGCTG 947
DB 1907 GAAAGATAGGCGGTATACACTGTGATGAAGAGAAATATCAATAATATTCGGCTG 1966
QY 948 GCCGCAAAATATTTAATCAATTGAATTCCTTCCACTAGC----- 987
DB 1967 GCCGCAAAATATTTAATCAATTGAATTCCTTCCACTAGCCTGTATATGCA 2026
QY 988 ----- 987
DB 2027 ACTGTACACTAACAAAAGTTTCAACAAAGATGTTCACTCTCATATTTTCCTTGTAT 2086
QY 988 -----GTTACGAAACAGCTCTAGTCAACATGACAGCATGGAATGTGGCCTT 1035
DB 2087 GTGTATCCATGATGACGAAACAGCTCTAGTCAACATGACAGCATGGAATGTGGCCTT 2146
QY 1036 CCCACCTTTTGTCTTTTACAGCCCGGTGAACTAGAGATGGAGCTTTTCAAGCAATA 1095
DB 2147 CCCACCTTTTGTCTTTTACAGCCCGGTGAACTAGAGATGGAGCTTTTCAAGCAATA 2206
QY 1096 GAAAGCTATGACCCAGATGACAGAGATGTTTACACAGTTAAAGAACT 1144
DB 2207 GAAAGCTATGACCCAGATGACAGAGATGTTTACACAGTTAAAGAACT 2255

RESULT 6
LOCUS AX037606 3896 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 30 from Patent WO0060095.
ACCESSION AX037606
VERSION AX037606.1 GI:11227020

KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 3896)
AUTHORS Banas,A., Stahl,U., Szyme,S., Lenman,M., Ronne,H. and Dahlqvist,A.
TITLE A new class of enzymes in the biosynthetic pathway for the production of triacylglycerol and recombinant dna molecules encoding these enzymes
JOURNAL Patent: WO 0060095-A 30 12-OCT-2000;
BASF PLANT SCIENCE GMBH (DE); BANAS ANTONI (PL); STAHL Ulf (SE); STYME STEN (SE); LENMAN MARI (SE); RONNE HANS (SE); DAHLQVIST ANDERS (SE)

FEATURES Location/Qualifiers

source 1..3896
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

Query Match 16.6%; Score 271.8; DB 6; Length 3896;
Best Local Similarity 80.0%; Pred. No. 2.7e-67;
Matches 375; Conservative 0; Mismatches 2; Indels 92; Gaps 1;

ORIGIN

768 TGAGGAACCTGCTCGGTGTTGTGTCGAATTCCTTTGCGTGCATTTGGCTTATGCCATT 827
DB 1787 TCAGGGAACCTGCTCGGTGTTGTGTCGAATTCCTTTGCGTGCATTTGGCTTATGCCATT 1846
QY 828 TTCAAAGATTGCAAGGGTGATACACATCTCGACGCAATTTTCTGGGGGTGCTGCAA 887
DB 1847 TTCAAAGATTGCAAGGGTGATACACATCTCGACGCAATTTTCTGGGGGTGCTGCAA 1906
QY 888 GAAAGATAGGCGGTATACACTGTGATGAAGAGAAATATCAATAATATTCGGCTG 947
DB 1907 GAAAGATAGGCGGTATACACTGTGATGAAGAGAAATATCAATAATATTCGGCTG 1966
QY 948 GCCGCAAAATATTTAATCAATTGAATTCCTTCCACTAGC----- 987
DB 1967 GCCGCAAAATATTTAATCAATTGAATTCCTTCCACTAGCCTGTATATGCA 2026
QY 988 ----- 987
DB 2027 ACTGTACACTAACAAAAGTTTCAACAAAGATGTTCACTCTCATATTTTCCTTGTAT 2086
QY 988 -----GTTACGAAACAGCTCTAGTCAACATGACAGCATGGAATGTGGCCTT 1035
DB 2087 GTGTATCCATGATGACGAAACAGCTCTAGTCAACATGACAGCATGGAATGTGGCCTT 2146
QY 1036 CCCACCTTTTGTCTTTTACAGCCCGGTGAACTAGAGATGGAGCTTTTCAAGCAATA 1095
DB 2147 CCCACCTTTTGTCTTTTACAGCCCGGTGAACTAGAGATGGAGCTTTTCAAGCAATA 2206
QY 1096 GAAAGCTATGACCCAGATGACAGAGATGTTTACACAGTTAAAGAACT 1144
DB 2207 GAAAGCTATGACCCAGATGACAGAGATGTTTACACAGTTAAAGAACT 2255

RESULT 7
LOCUS AC003027 119914 bp DNA linear PLN 30-OCT-2002
DEFINITION Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence.
ACCESSION AC003027
VERSION AC003027.1 GI:4079614
KEYWORDS HMG.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 119914)
AUTHORS Federapfel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Alatafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremetskaia,I., Kim,C., Ient,C., Li,J., Liu,S., Luvos,S., Schwartz,J., Shinn,P., Tortum,M., Vysotskaia,V.S., Walker,M., Yu,G., Becker,J., Theologis,A. and Davis,R.W.
TITLE Arabidopsis thaliana (thale cress)

REFERENCE 2 (bases 1 to 119914)
AUTHORS Federapfel,N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R., Au,M., Araujo,R., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y., Oj,O., Osborne,B.I., Shinn,P., Sun,H., Tortum,M., Vysotskaia,V., Yu,G., Becker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission

JOURNAL Submitted (22-OCT-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo Alto, CA 94304, USA
REFERENCE 3 (bases 1 to 119914)

AUTHORS Federapfel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Alafifi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremencskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Lueros, S., Schwartz, J., Shim, P., Toriumi, M., Vyotekala, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.

TITLE Direct Submission

JOURNAL Submitted (30-DEC-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

REFERENCE 4 (bases 1 to 119914)

AUTHORS Federapfel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Alafifi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremencskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Lueros, S., Schwartz, J., Shim, P., Toriumi, M., Vyotekala, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.

TITLE Direct Submission

JOURNAL Submitted (30-JAN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT On Dec 30, 1998 this sequence version replaced gi:2734094. Bases 1-9262 of clone F21M1 overlap with bases 68998-78259 of 'TAMU' BAC clone F20D22 (AC002411) and bases 119525-119914 of clone F21M1 overlap with bases 1-389 of 'TAMU' BAC clone F21B7 (AC002560).

e-mail for correspondence: arab@sequence.stanford.edu

Genes with similarity to proteins in the databases are described as 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/section/index.html>), GENSCAN (Chris Burge, <http://genomic.stanford.edu/~chris/GENSCAN.html>), Fexa (V.Solovayev & A.Salamov, Sanger Centre, <http://genomic.sanger.ac.uk/>), and NetPlantGene (S.M. Hebsgaard, et al., CMS, Technical University of Denmark, <http://www.cbs.dtu.dk/NetPlantGene.html>).

FEATURES

SOURCE Location/Qualifiers

1..119914

/organism="Arabidopsis thaliana"

/mol_type="Genomic DNA"

/cultivar="Columbia"

/db_xref="taxon:3702"

/chromosome="1"

/clone="F21M1"

1..9262

/note="Overlap with bases 68998-78259 of 'IGF' BAC clone F21M1."

misc_feature

1..7000

/note="Proteins in this region are annotated in the F21M1 entry, AC002411."

7684..10913

/gene="F21M1.1"

join(7684..7665,7965..8027,8122..8160,8250..8381,8458..8728,8875..9893,10003..10256,10344..10410,10501..10551,10685..10781,10885..10913)

/gene="F21M1.1"

/note="Hypothetical protein"

/codon_start=1

/protein_id="AADI0665.1"

/db_xref="GI:4204284"

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gene

13033..14514

/gene="F21M1.2"

join(13033..13488,13717..13926,14139..14514)

/gene="F21M1.2"

join(13061..13488,13717..13926,14139..14516)

/gene="F21M1.2"

/note="Similar to acid phosphatase, Location of ESTs 110C2T7, gb|742036, and 110C3XP, gb|A1100245"

/codon_start=1

/protein_id="AADI0666.1"

/db_xref="GI:4204285"

/translation="MDRMTFLSLTILAGVVSAGDMNINOLRGLGSSONGYIV KGIKTDLKGCESRIVNEVHNTRKFDVPEQCSYSHKDYTSQYKODVARTDEVI LHFQSMCSKSCDGMALFDIDTLSTPIYHKNGPFGEGELNSTKEDWLOQKK APAPVPMKKLVHYDIRERGIKIFLISREKYLRSATVNLIOAGYGMNMLRLEDO QKEVQYKSEKRKMLMELGYVMGWMDQNSFAGCPLPRTPFLPNSIYVA"

gene

complement(114004..16362)

/gene="F21M1.3"

complement(join(14004..14312,14565..14641,14787..15831,15906..16006,16327..16362))

/gene="F21M1.3"

complement(join(14567..14641,14787..15831,15906..16006,16327..16362))

/gene="F21M1.3"

/note="Unknown protein, Location of ESTs 40C3TT, gb|AA728590 and 40C3T7, gb|704573"

/codon_start=1

/protein_id="AADI0667.1"

/db_xref="GI:4204286"

/translation="MDQISGNTHHEKLSVETAPRHLLNDRVHTVEIPKASVPIRE ICDAEKGCPSTISRKRVTFSKVKTYEHVVSSEYVLSSEKNEVESESRKSSK TDDIILIVANSSGSPENHRKNCRESDDIDEDEDCSDSDLEDEEYSDVGSB ESSEIDEMTDKDVSKSGTDSGRDGPVPTSESDPRGHQDMTEKQSLDHLLEY FESYDAAHNTPESTEOAANKVDIRASIEQPSAAKRIIGDIFDESSPNPTDPE TLRLMSLSLSDPDTDVAKONHOMVRFSPVLTYSFPLCRSNLRCVLFECVOOLPK SHTQDSKRRKRDITASAMENHLKVPRENNLMKSDADIDONGCSANSQDLEKIS KALEQTSNNTTGGFCOSAVSEATGMLHSRQRPVADGIFRSNVLHVASACTEMA POUYVEDTTLCKLAEELARGMKICTGSCGKGAALGFCVSCRSYHVPACFELVIRCG WDYEDPFLICPAHSVYKFPNEKSGHRSRLEPLKIPABICSELEOPAPFKEVLVCG SALSXDKLMESLAVRFNATISRYNPSVYHVASIDEKACRTRLKVLMLGILNGKA IINAAMKASIKASQVDEDEPEFIOITOGCQDPKAPRLAETNNKPLFEGCLFYFP GDPLYKGYKEDLQNLVKYAGGTIINTLEBELGAESSNNVNDORSSITVYINIDPRHCAL GEEVTIILWQRANDALASQTSRLVGHVHWLESIAQIKLHPVIG"

gene

22102..22102

/gene="F21M1.5"

join(20752..20994,21362..21497,21596..21740,21825..21994,22102..22178,22542..22758,22920..23064,23343..23442,23599..23693,24021..24072,24227..24298,24441..24647)

/gene="F21M1.5"

/note="Hypothetical protein"

/codon_start=1

/protein_id="AADI0668.1"

/db_xref="GI:4204287"

/translation="WGANSSKSVTASFTVIAVFLICGGRTRAVEDTEPHGYSLSGI

ROIRAMEELMDVIGIDPNDSDLMKPFDCLOGSFRCNNKRSSTMTQILINKA"

13033..14514

/gene="F21M1.2"

join(13033..13488,13717..13926,14139..14514)

/gene="F21M1.2"

join(13061..13488,13717..13926,14139..14516)

/gene="F21M1.2"

/note="Similar to acid phosphatase, Location of ESTs 110C2T7, gb|742036, and 110C3XP, gb|A1100245"

/codon_start=1

/protein_id="AADI0666.1"

/db_xref="GI:4204285"

/translation="MDRMTFLSLTILAGVVSAGDMNINOLRGLGSSONGYIV KGIKTDLKGCESRIVNEVHNTRKFDVPEQCSYSHKDYTSQYKODVARTDEVI LHFQSMCSKSCDGMALFDIDTLSTPIYHKNGPFGEGELNSTKEDWLOQKK APAPVPMKKLVHYDIRERGIKIFLISREKYLRSATVNLIOAGYGMNMLRLEDO QKEVQYKSEKRKMLMELGYVMGWMDQNSFAGCPLPRTPFLPNSIYVA"

gene

complement(114004..16362)

/gene="F21M1.3"

complement(join(14004..14312,14565..14641,14787..15831,15906..16006,16327..16362))

/gene="F21M1.3"

complement(join(14567..14641,14787..15831,15906..16006,16327..16362))

/gene="F21M1.3"

/note="Unknown protein, Location of ESTs 40C3TT, gb|AA728590 and 40C3T7, gb|704573"

/codon_start=1

/protein_id="AADI0667.1"

/db_xref="GI:4204286"

/translation="MDQISGNTHHEKLSVETAPRHLLNDRVHTVEIPKASVPIRE ICDAEKGCPSTISRKRVTFSKVKTYEHVVSSEYVLSSEKNEVESESRKSSK TDDIILIVANSSGSPENHRKNCRESDDIDEDEDCSDSDLEDEEYSDVGSB ESSEIDEMTDKDVSKSGTDSGRDGPVPTSESDPRGHQDMTEKQSLDHLLEY FESYDAAHNTPESTEOAANKVDIRASIEQPSAAKRIIGDIFDESSPNPTDPE TLRLMSLSLSDPDTDVAKONHOMVRFSPVLTYSFPLCRSNLRCVLFECVOOLPK SHTQDSKRRKRDITASAMENHLKVPRENNLMKSDADIDONGCSANSQDLEKIS KALEQTSNNTTGGFCOSAVSEATGMLHSRQRPVADGIFRSNVLHVASACTEMA POUYVEDTTLCKLAEELARGMKICTGSCGKGAALGFCVSCRSYHVPACFELVIRCG WDYEDPFLICPAHSVYKFPNEKSGHRSRLEPLKIPABICSELEOPAPFKEVLVCG SALSXDKLMESLAVRFNATISRYNPSVYHVASIDEKACRTRLKVLMLGILNGKA IINAAMKASIKASQVDEDEPEFIOITOGCQDPKAPRLAETNNKPLFEGCLFYFP GDPLYKGYKEDLQNLVKYAGGTIINTLEBELGAESSNNVNDORSSITVYINIDPRHCAL GEEVTIILWQRANDALASQTSRLVGHVHWLESIAQIKLHPVIG"

gene

22102..22102

/gene="F21M1.5"

join(20752..20994,21362..21497,21596..21740,21825..21994,22102..22178,22542..22758,22920..23064,23343..23442,23599..23693,24021..24072,24227..24298,24441..24647)

/gene="F21M1.5"

/note="Hypothetical protein"

/codon_start=1

/protein_id="AADI0668.1"

/db_xref="GI:4204287"

/translation="WGANSSKSVTASFTVIAVFLICGGRTRAVEDTEPHGYSLSGI

IIPEFASITQLRAMSILDCPYPLDENPLDLVWLDITTKLLSAVNCNFKMCLVDLPYNQD
HPECKSRDSDGSLATLELDPGITTPLSTVWKEMLKMCVEGIEENALVAAPYDRLS
PTKLEERLDYFHKHLKTPETALKLRGSPSIYFAHMGNNVPRYFLFEMLRLEAPKHYL
KMLDHIHAYFAVGA PILGSVAEAKSTISCTGTFGLPVESEGARLLISNPFASISIMMP
SKNCKGDTFTWTHBSGAAKKDKRYTHCDEBERYGKSGWPTNITINISIPASBELA
DGTLEKALIEDYDPSKMLHDKKYVPPFVRLNLRSLGFLYHODPVNPLTPM
ERPPIKNVFCIYGAHLKTEVGYFAPSGKPPDMMIITDIIYETEGSLVSSGTVDG
NAGPTGDETVYHSLSNCKMLGPKNITMAPOLLIIGIKIQOPHEDSDVHELVND
HEHSGDITAMTKAPRVKVIYTFEYDESEI PGKRTAVWELDKSGY"

gene
27777..28734
/gene="F21M11.6"
/db_xref="GI:4204289"
/protein_id="AA010670.1"
/cdon_start=1
/note="unknown protein; location of ESTs 203124T7,
gb|H76794 and 203124XP, gb|AA605510"

mRNA
27777..28734
/gene="F21M11.6"
28007..28465
/gene="F21M11.6"

CDS
complement (29264..32033)
/gene="F21M11.7"
complement (29264..31015,31312..31414,31484..31587,
31664..31764)

Query Match 16.6%; Score 271.8; DB 8; Length 119914;
Best Local Similarity 80.0%; Pred. No. 36-67; Indels 92; Gaps 1;
Matches 375; Conservative 0; Mismatches 2;

gene
22538 TCAGGAACTGCTCGGTTGTGTCATTCCTTTGCGTGTGCTATGCGCTTATGCCATT 22537
768 TGAGGAACTGCTCGGTTGTGTCATTCCTTTGCGTGTGCTATGCGCTTATGCCATT 827
828 TTCAAGAACTGCAAGGTGATTAACAATCTCTGACGCAATTTTCTGGGGGTGCTGCAAA 887
22598 TTCAAGAACTGCAAGGTGATTAACAATCTCTGACGCAATTTTCTGGGGGTGCTGCAAA 22657
888 GAAAGATTAAGCGCGCTTATCACTGATGAAGAGAAATTCATCAATAATTTCTGGCTG 947
22658 GAAAGATTAAGCGCGCTTATCACTGATGAAGAGAAATTCATCAATAATTTCTGGCTG 22717
948 GCCGCAATATTTAATTAATGAAATTCCTTCCACTAGC----- 987
22718 GCCGCAATATTTAATTAATGAAATTCCTTCCACTAGCCTGATGATATGCA 22777
988 ----- 987
22778 ACTGTACACTTAACAAAGTTTCACCAAGATGTTCACTCATATTTGTTCTTTGAT 22837
988 -----GTTACGAAACAGCTCTGATCAATGACACGACATGGAATGTGGCTT 1035
22838 GTGTATCATCATGTTACGAAACAGCTCTGATCAATGACACGACATGGAATGTGGCTT 22897
1036 CCCACCTTTTGTCTTTTACAGCGCGGTGAATGAGATGGGACTCTTTTCAAGCAATA 1095
22898 CCCACCTTTTGTCTTTTACAGCGCGGTGAATGAGATGGGACTCTTTTCAAGCAATA 22957
1096 GAAAGCTATGACCCAGATGACAAAGATGTTTACACCAAGTTAAGAGT 1144
22958 GAAAGCTATGACCCAGATGACAAAGATGTTTACACCAAGTTAAGAGT 23006

RESULT 8
AX090328 AX090328 328 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 21 from Patent WO0116308.
ACCESSION AX090328
VERSION AX090328.1 GI:13444194
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
1 Laessle, M. and van Eenennaam, A.
TITLE Plant sterol acyltransferases
Patent: WO 0116308-A 21 08-MAR-2001;
MONSANTO COMPANY (US)

FEATURES
SOURCE location/Qualifiers
1..328
/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

ORIGIN

Query Match 10.7%; Score 176.2; DB 6; Length 328;
Best Local Similarity 79.0%; Pred. No. 1.66-39; Indels 1; Gaps 1;
Matches 222; Conservative 0; Mismatches 58;

QY 238 ACTAAGCTTCTTCTGCTGTCACAGCTGTTTAACTATGCTAGATCTTATAT 297
DB 35 ACATTGCTTTCTCTGCGGTAAATGCTGCTTAAATGCAATGCTGTTAAT 94
QY 298 CAACAGACCATCCCGAGTGAAGTACAGGCTGACAGTGTCTTTGACCAATCAGAA 357
DB 95 CAGATAGACCATCCCGAGTGAAGTACAGGCTGATGATGTC-TTCGCAATTCAGAG 153
QY 358 TTGATCCAGTTCATTAACAGGCTCTTCTTCTACTGCTCGGAAGAGTGGCTTAAGGG 417
DB 154 CTGACCTGCTTATTAACAGGCTCTTCTTCTGATGAAAGATGGCTAAAGG 213
QY 418 TGTGTGAGTTTGTGATGAAGCAATATGTCGCTTCCATGATGAGATG 477
DB 214 TGTGTGAGTTTGTGATGAAGCAATATGTCGCTTCCATGATGAGATG 273
QY 478 TCACCAACCAATGGAAGAGCGTGAACCTTACTTTCACAA 518
DB 274 CCCCATCAATGCTGAGAGAGAGATCTGATCTTTCACAA 314

RESULT 9
AP006356/c 93398 bp DNA linear PLN 22-JUL-2003
LOCUS AP006356
DEFINITION Locus corniculatus var. japonicus genomic DNA, chromosome 6,
clone:ljt06108, TM0082b, complete sequence.
ACCESSION AP006356
VERSION AP006356.1 GI:31580987
KEYWORDS HTG.
SOURCE Locus corniculatus var. japonicus (Locus japonicus)
ORGANISM Locus corniculatus var. japonicus
Locus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotsee;
Locus.

REFERENCE
1 Asamiya, B., Kato, T., Sato, S., Nakamura, Y., Kaneko, T. and Tabata, S.
TITLE Structural Analysis of a Lotus japonicus Genome. IV. Sequence
Features and Mapping of seventy-three TAC clones which cover the
7.5 Mb Regions of the genome
DNA Res. (2003) In press
2 (bases 1 to 93398)
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Direct Submission
Submitted (07-MAY-2003) Shusei Sato, Kazusa DNA Research Institute,
Department of Plant Gene Research, 2-6-7 Kazusa-Kamatari, Kisarazu,
Chiba 292-0818, Japan (E-mail: sato@kazusa.or.jp,
URL: http://www.kazusa.or.jp/, Tel: 81-438-52-3935 (ex. 2337),
Fax: 81-438-52-3934)

FEATURES
source location/Qualifiers
1..93398
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/mol_type="genomic DNA"
/variety="japonicus"

ORIGIN	/db_xref="taxon:34305" /chromosome="6" /clone="LjT06108" /clone1b="LjT11library" /note="TM0082b, a part of TAC clone:TM0082.-synonym: Lotus japonicus"			
Query Match	7.2%;	Score 118;	DB 8;	Length 93398;
Best Local Similarity	79.9%;	Pred. No. 1.6e-22;		
Matches 139;	Conservative	0;	Mismatches 35;	Indels 0; Gaps 0;
Qy	522	CAAGTTCACCTTGAACCTGCTTAAACCTCCGTGGCGCCCTTCTATAGATTGTCCTCA	581	
Db	32553	CAGATTGACATTGGAACCTGCTTAAACCTTGAAGTGGCCCTCTTATAGTTTGGCCCA	32494	
Qy	582	TTCAATGGATATATATGCTTCAGATACCTTCTGGAATGGCTGAGCTAGAAATGCACC	641	
Db	32493	TTCAATGGATATATACGTTTTCCTTATTTCTTGAGTGGTTGAGCTAGACATAGCAC	32434	
Qy	642	AAACATTATTTGAAAGTGGCTTGAATCAGCATATTCATGCTTATTTGCTGTGG	695	
Db	32433	AAACATTATTTGCAATGGCTGATCAACATATTCACGATATTTTGTGCTTGG	32380	
RESULT 10				
AP004120/C	LOCUS	118192 bp	DNA	linear
DEFINITION	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,			
ACCESSION	AP004120			
VERSION	AP004120.3 GI:47847857			
KEYWORDS	Oryza sativa (japonica cultivar-group)			
ORGANISM	Oryza sativa (japonica cultivar-group)			
REFERENCE	Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nippondare (GAJ) genomic DNA, chromosome 2, BAC clone:OU1293 E04 Published Only in Database (2001) 2 (bases 1 to 118192) Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission Submitted (29-AUG-2001) Takui Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kamondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rjp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468) On Jun 1, 2004 this sequence version replaced gi:34740243. Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mt.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://opal.biology.gatech.edu/GeneMark/), GlimmerX (http://www.tigr.org/tcb/glimmer/glmr_form.html), RiceHMM (http://rjp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), slm4 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The genomic sequence was searched against NCBI Nonredundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologs of the coding regions were searched against NCBI Nonredundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or			

FEATURES	location/Qualifiers			
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misc_feature				
gene				
mRNA				
CDs				


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16996. .17067,17265. .17368,18290. .18363,18462. .18545,
19079. .19166,19280. .19341,19675. .19748,19971. .20078,
20180. .20244,20814. .20927,21141. .21240,21337. .21390,
21469. .21825)
/gene="OJ1293_E04.4-1"
/note="supported by full-length cDNA(s) : AK100446"
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18462. .18545,19079. .20078,20814. .20860)
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non-coding transcript
probably inactive due to including stop codon(s) in CDS"
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20814. .20927,21141. .21240,21337. .21390,21469. .21564)
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contains full-length cDNA(s) : AK100446,AK058270"
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/translation="MARCKLKDSEVENAVATDGGSYVDLFPVIGAGSGGSGRSTASAF
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GDINPCKRLLENKTOEIVRLNGYQIRLNGSLGSMYSGASVLPDEPDANCPMBEIN
QRYTAKHLIATGSRQKVNTPGKELATISSEALSLERAPRAVILGGGYATVPASFI
WKGGAHVDFYRKELPLRGPDDEKRTVAANLSEGRRLHPGNTLSLSTADGIV
VTDGSEIIADVLPATGRTNSQRLNLEAGVENDGAIKVDYSSTSPNIMAWG
DVTNRINLPALMEATGCTKTPGQPTKPDYDPCAVASIPLSVVGSEDOALB
EAKSDVLYVTSFNPMPKNSIKRQKTKMKLVDSMDKVGAGSMCGDPAEIIQMA
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complement(join(27410. .27558,29301. .29382))
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31777. .33484
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/note="supported by full-length cDNA(s) : AK107210"
31845. .33336
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/note="contains full-length cDNA(s) : AK107210"
/codon_start=1
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synthase 1"
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/db_xref="GI:47847862"
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DKVTTELAGATIEENKRIGLBEYRLLKQVUNGSGHRTYSPNVLDARDCPTLRD
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AYNSGMCSSAGLVSVDLARVVMLTRPTMLVLTSSCAFNWVTGDSMWLGLCPL
RCGAAALLTNDPAFRSRAKMLRCLVRAHICAHDDAHAAVHREDADGRIGVLSKA
LPKAAVRAFTENLQRLAPRIIPAGELARFAARLLRLKILRRKAAAGAAKINFTGV

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Query Match      6.9%  Score 113.4;  DB 8;  Length 118192;
Best Local Similarity 77.1%;  Pred. No. 3.6e-21;
Matches 138;  Conservative 0;  Mismatches 41;  Indels 0;  Gaps 0;

gene
misc_feature

517 AACCTCAAGTTGACCTTGAAGTCTTAAACTCCGCGGCGCCCTTATAGTATT 576
64553 AACGCAAGTTAACTTTGAAAGTCAATGAACTTGAGAGAGCGCTTTTGTGTT 64494
577 GCCCATCAATGGGTAATATGCTTCAATCTTCTGAAATGCTGAGGCTGAAATT 636
64493 GCTCATTCATCGGTAATATGCTTCTGCACTTCTGAAATGCTTGAACCTGAAATC 64434
637 GCACCAAAACATTTTGAAGTGCGCTGATCAGCATTCATGCTTATTTGCTGTTGG 695
64433 GCTCCAAAGCATTAATCCAGTGCCTGACGACATATACATGCAATCTTGCACTGG 64375

RESULT 11
LOCUS      AP005691/c      147123 bp      DNA      linear      PLN 02-JUN-2004
DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,
ACCESSION  AP005691
VERSION     AP005691.3  GI:47848524
KEYWORDS
SOURCE      ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group) Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eubharitoidae; Oryzae; Oryza.

REFERENCE
1 Sasaki, T., Matsumoto, T. and Katayose, Y.
Oryza sativa nipponbare (Ga3) genomic DNA, chromosome 2, BAC
clone:OSUNBA0053L11
Published Only in Database (2002)
2 (bases 1 to 147123)
Direct Submission
Sasaki, T., Matsumoto, T. and Katayose, Y.
Submitted (05-SEP-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://exp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
On Jun 1, 2004 this sequence version replaced gi:38564216.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
(http://www.softberry.com/), GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark/), Glimmer
(http://www.tigr.org/cdb/glimmer/glmr.fom.html), RiceHMM
(http://exp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://bioinformatics.iastate.edu/cgi-bin/isp.cgi), sim4
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The
genomic sequence was searched against NCBI NonRedundant Protein
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
sequence database at RGP or DDBJ. Protein homologies of the coding
regions were searched against NCBI Nonredundant Protein database
with BLASTP. ESTs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
Full-length cDNAs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without

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/translation="MEVKKPVGNISQICVEGVQVLEILNIGESLWVVKHGIACRDVEVA
KDVVGVGVKLAJ"
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/gene="OSJNB0053111.9"
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/gene="OSJNB0053111.9"
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predicted by GlimmerM
this category is not included in IRGSP standard"

Query Match 6.9%; Score 113.4; DB 8; Length 147123;
Best Local Similarity 77.1%; Pred. No. 3.6e-21;
Matches 138; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Oy 517 AAGCTCAAGTTGACCTTGAAGCTCTTAAACCTCGTGGGCGCTTCTAATGATTT 576
Db 126651 AACTGCAGTTTAACTTTGAAACCTGATTAACCTGAGAGGCGCTTCTTATGTTT 126592
Oy 577 GCCCATCAATGGGTAATATGTCCTTCAGATACCTTTCTGAATGCTGAGGCTAGAAATT 636
Db 126591 GCTATTCATGGGTAATATGTCCTTCAGATACCTTTCTGAATGCTGAGGCTAGAAATT 126532
Oy 637 GCACCAAAACATTTATTTGAGTGGCTTATCAGCATTCATGCTTTATTTGGCTTTGG 695
Db 126531 GCTCCCAAGCATTCATCCGATGCTTACGCAACATATATGATGATCTTTGCAAGTTGG 126473

RESULT 12
AP004882/c 158971 bp DNA linear HTG 23-MAR-2002
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) chromosome 2 clone P0511E12,
*** SEQUENCING IN PROGRESS ***.

ACCESSION
AP004882
KEYWORDS
HTG; HTGS; PHASE2.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitoidae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
1 Sasaki, T., Matsumoto, T. and Yamamoto, K.
Oryza sativa nippondare (GAJ) genomic DNA, chromosome 2, PAC
clone: P0511E12
JOURNAL
REFERENCE
AUTHORS
TITLE
2 (bases 1 to 158971)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submision
Submitted (20-MAR-2002) Takui Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rsg.dna.affrc.go.jp/
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
NOTE: It currently consists of 1 contig. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

COMMENT
FEATURES
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1. 158971
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
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ORIGIN

Query Match 6.9%; Score 113.4; DB 2; Length 158971;
Best Local Similarity 77.1%; Pred. No. 3.6e-21;
Matches 138; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Oy 517 AAGCTCAAGTTGACCTTGAAGCTCTTAAACCTCGTGGGCGCTTCTAATGATTT 576
Db 58238 AACTGCAGTTTAACTTTGAAACCTGATTAACCTGAGAGGCGCTTCTTATGTTT 58179
Oy 577 GCCCATCAATGGGTAATATGTCCTTCAGATACCTTTCTGAATGCTGAGGCTAGAAATT 636
Db 58178 GCTATTCATGGGTAATATGTCCTTCAGATACCTTTCTGAATGCTGAGGCTAGAAATT 58119
Oy 637 GCACCAAAACATTTATTTGAGTGGCTTATCAGCATTCATGCTTTATTTGGCTTTGG 695
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RESULT 13
BD271624 709 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
Novel class enzyme in biosynthesis pathway of triacylglycerol
production and recombinant DNA molecule encoding the enzyme.
ACCESSION
BD271624
VERSION
BD271624.1 GI:33081392
KEYWORDS
JP 2002541783-A/9.
SOURCE
Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 709)
AUTHORS
TITLE
Dahlqvist, A., Stahl, U., Lemman, M., Banas, A., Ronne, H. and Stymne, S.
Novel class enzyme in biosynthesis pathway of triacylglycerol
production and recombinant DNA molecule encoding the enzyme
Patent: JP 2002541783-A 9 10-DEC-2002;
JOURNAL
COMMENT
OS Lycopersicon esculentum (tomato)
PN JP 2002541783-A/9
PD 10-DEC-2002
PF 28-MAR-2000 JP 2000609586
PR 01-APR-1999 EP 99106656.4, 10-JUN-1999 EP 99111321.8 PR
PI 07-FEB-2000 US 60/180687
PI ANDERS DAHLQVIST, ULF STAHL, MARIT LENMAN, ANTONI BANAS PI
, HANS RONNE, STEN STYME
PC C12N15/09, A01H5/00, C12N1/19, C12N5/10, C12N9/10, C12P7/64// PC
(C12P7/64, C12R1:645), (C12P7/64, C12R1:91), C12N5/00, C12N5/00 CC
Novel class enzyme in biosynthesis pathway
of triacylglycerol
production
CC and recombinant DNA molecule encoding the enzyme FH Key
Location/Qualifiers
FT source 1.709
/organism="Lycopersicon esculentum (tomato)"
/mol_type="genomic DNA"
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FEATURES
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1. 709
/organism="Lycopersicon esculentum"
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Query Match 6.7%; Score 110.4; DB 6; Length 709;
Best Local Similarity 74.5%; Pred. No. 2.3e-20;
Matches 152; Conservative 0; Mismatches 51; Indels 1; Gaps 1;

Oy 1426 CTCGACCTTAAGTTAATACATACATGCTCCCAAGCAACATGAGGAGGATTA 1485
Db 1 CTGGGGGCCAAAGGAACATTAACAGACACACAGTCAGAGCATGAT-GTTCAAGATTA 59
Oy 1486 CATGTGAACATTAATGTTGATCAGACATGGGTCAGACATCAATGATTAATACATGACAAA 1545
Db 60 CAAGTGATCTTAATATATGAGCATCAACATGATGATATCATTTCCAAATATACAAAG 119
Oy 1546 GCACCAAGGTTAATGATACATACCTTTATGAAGACTCTGAGAGCATTCGGGGAAGAGA 1605

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Db      120 TTACTTAAATGATGATACATTAACCTATATATGAGGATCTGAAAAGTTTCAGGGACAAGA 179
QY      1606 ACCGCACTCTGGAGCTTGATAAA 1629
Db      180 ACAGCAGTTTGGAGCTTGATAAA 203

RESULT 14
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LOCUS   709 bp, DNA, linear, PAT 17-JUL-2003
DEFINITION Novel class enzyme in biosynthesis pathway of triacylglycerol
production and recombinant DNA molecule encoding the enzyme.
VERSION BD271634.1 GI:33081402
KEYWORDS JP 2002541783-A/19.
SOURCE   Lycopersicon esculentum (tomato)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 709)
AUTHORS Dahlqvist, A., Stahl, U., Lemman, M., Banas, A., Ronne, H. and Stymne, S.
TITLE Novel class enzyme in biosynthesis pathway of triacylglycerol
production and recombinant DNA molecule encoding the enzyme
JOURNAL Patent: JP 2002541783-A 19 10-DEC-2002;
BASF PLANT SCIENCE GMBH
COMMENT OS Lycopersicon esculentum (tomato)
PN JP 2002541783-A/19
PD 10-DEC-2002
PF 28-MAR-2000 JP 2000609586
PR 01-APR-1999 EP 9910656.4, 10-JUN-1999 EP 9911121.8 PR
PT 07-FEB-2000 US 60/180687
PI ANDERS DAHLQVIST, ULF STAHL, MARIT LENMAN, ANTONI BANAS PI
HANS RONNE, STEN STYME
PC C12N15/09, A01H5/00, C12N1/19, C12N5/10, C12N9/10, C12P7/64// PC
(C12P7/64, C12R1:645), (C12P7/64, C12R1:91), C12N15/00, C12N5/00 CC
Novel class enzyme in biosynthesis pathway
of triacylglycerol
production
CC and recombinant DNA molecule encoding the enzyme FH Key
location/Qualifiers
FT source 1..709
FEATURES
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1..709
/mol_type="genomic DNA"
/db_xref="taxon:4081"
ORIGIN
Query Match 6.7%; Score 110.4; DB 6; Length 709;
Best Local Similarity 74.5%; Pred. No. 2.3e-20;
Matches 152; Conservative 0; Mismatches 51; Indels 1; Gaps 1;

QY 1426 CTCGACCTTAAAGTTAACTAATCAATGCGTCCCGCCAGCAACAGATGAAAGCAGCTA 1485
Db 1 CTGGGGCCAAAAGTAAACATTAACAGACACCAAGTCAGAGCATGAT-GTTCAGATGTA 59
QY 1486 CATGTGAACCTAAATGTTGATCATGAGCATGGGTGAGCATCATAGCTAATACATGACAAA 1545
Db 60 CAAGTCATCTTAATATATAGAGCATCAACATGGTGAAGATATCATATCCCAATATGACAAAG 119
QY 1546 GCACCAAGGTTAATGATACATAAAGCTTTATGAAGACTCTGAGAGCATTCGGGGAGAAGA 1605
Db 120 TTACTTAAATGATGATACATTAACCTATATATGAGATTCGAAAAGTTTTCAGGGACAAGA 179
QY 1606 ACCGCACTCTGGAGCTTGATAAA 1629
Db 180 ACAGCAGTTTGGAGCTTGATAAA 203

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RESULT 15

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AX037588
LOCUS   709 bp, RNA, linear, PAT 16-NOV-2000
DEFINITION Sequence 12 From Patent WO0060095.
ACCESSION AX037588
VERSION AX037588.1 GI:11227007
KEYWORDS
SOURCE   Lycopersicon esculentum (tomato)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1
AUTHORS Banas, A., Stahl, U., Stymne, S., Lemman, M., Ronne, H. and Dahlqvist, A.
TITLE A new class of enzymes in the biosynthetic pathway for the
production of triacylglycerol and recombinant dna molecules
encoding these enzymes
JOURNAL Patent: WO 0060095-A 12 12-OCT-2000;
BASF PLANT SCIENCE GMBH (DE) ; BANAS ANTONI (PL) ; STAHL ULF (SE) ;
STYME STEN (SE) ; LENMAN MARIT (SE) ; RONNE HANS (SE) ; DAHLQVIST
ANDERS (SE)
FEATURES
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1..709
/mol_type="unassigned RNA"
/db_xref="taxon:4081"
ORIGIN
Query Match 6.7%; Score 110.4; DB 6; Length 709;
Best Local Similarity 74.5%; Pred. No. 2.3e-20;
Matches 152; Conservative 0; Mismatches 51; Indels 1; Gaps 1;

QY 1426 CTCGACCTTAAAGTTAACTAATCAATGCGTCCCGCCAGCAACAGATGAAAGCAGCTA 1485
Db 1 CTGGGGCCAAAAGTAAACATTAACAGACACCAAGTCAGAGCATGAT-GTTCAGATGTA 59
QY 1486 CATGTGAACCTAAATGTTGATCATGAGCATGGGTGAGCATCATAGCTAATACATGACAAA 1545
Db 60 CAAGTCATCTTAATATATAGAGCATCAACATGGTGAAGATATCATATCCCAATATGACAAAG 119
QY 1546 GCACCAAGGTTAATGATACATAAAGCTTTATGAAGACTCTGAGAGCATTCGGGGAGAAGA 1605
Db 120 TTACTTAAATGATGATACATTAACCTATATATGAGATTCGAAAAGTTTTCAGGGACAAGA 179
QY 1606 ACCGCACTCTGGAGCTTGATAAA 1629
Db 180 ACAGCAGTTTGGAGCTTGATAAA 203

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Search completed: November 9, 2004, 02:27:08
 Job time : 7042 secs

OY 689 CTGTTGAGCTCTCTTCTGTTGTTGAGCATCAATCTACTCTCTGCTGTA 748
Db 1181 ATATTAGTGATCTTCTTTGGGTACCAAGGCTATCCAGCATTAATTTCTGGTGA 1240
OY 749 CG 750
Db 1241 TG 1242

RESULT 2
US-08-916-421B-1
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Built et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc_feature

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/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1119881)..(1119881)
/ OTHER INFORMATION: n equals a, t, c, or g
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/ OTHER INFORMATION: n equals a, t, c, or g
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/ LOCATION: (1310988)..(1310988)
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/ OTHER INFORMATION: n equals a, t, c, or g
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/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1349491)..(1349491)
/ OTHER INFORMATION: n equals a, t, c, or g
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/ OTHER INFORMATION: n equals a, t, c, or g
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/ OTHER INFORMATION: n equals a, t, c, or g
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/ LOCATION: (1637998)..(1637998)
/ OTHER INFORMATION: n equals a, t, c, or g
/ NAME/KEY: misc.feature
/ LOCATION: (1664854)..(1664854)
/ OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
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Query Match 2.5%; Score 40.6; DB 4; Length 1664976;
Best Local Similarity 47.8%; Pred. No. 1.2;
Matches 118; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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OY 330 TGACGCTGCTTTTACGACCATACAGAAATGGATCCAGGTTACATPAACAGTCTCTTC 389
DB 1220217 TGGTGTGTTGTGTGTGCTTTCATGTCATTTGGAGCTATPAGAATTGATGAGTAGC 1220276
OY 390 TACTGTGGAAGAAGTGGCTTAAGTGTGTTGATGTTGATPAGAAGCAATGCAAT 449
DB 1220277 GATTAATGTAATGATGATGTTATPAGAAGATGTTGCAAGAAGTATGTCGCAAC 1220336
OY 450 TGTCCCTGTCATTCATGATGAGATTGACCAACCAATGGAAGAGCGTACCTTTA 509
DB 1220337 AGGACGTTATTAACAACCTTGAAGAAATATTAATATAAACAATAACGTAATPA 1220396
OY 510 CTTTACAAGCTCAAGTTGACCTTTGAAATGCTTTAAATCTCGTGGCGGCGCTTAT 569
DB 1220397 ATTATATAGCTTACTTACTTATGCAAAATGCAAAATATTCCTTAATTTT 1220456
OY 570 AGTATTT 576
DB 1220457 CATAATT 1220463
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RESULT 3
US-09-692-570-1
Sequence 1, Application US/09692570
Patent No. 6797466
GENERAL INFORMATION:
APPLICANT: Built et al.

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/ TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
/ Patent No. 6797466
/ TITLE OF INVENTION: jannaschi
/ FILE REFERENCE: PB275C1
/ CURRENT APPLICATION NUMBER: US/09/692,570
/ CURRENT FILING DATE: 2003-01-14
/ PRIOR APPLICATION NUMBER: US 60/024,428
/ PRIOR FILING DATE: 1996-08-22
/ PRIOR APPLICATION NUMBER: US 08/916,421
/ PRIOR FILING DATE: 1997-08-22
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 1664976
/ TYPE: DNA
/ ORGANISM: Methanococcus jannaschi
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (28222)..(28222)
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Query Match      2.5%; Score 40.6; DB 4; Length 164976;
Best Local Similarity 47.8%; Pred. No. 1.2;
Matches 118; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY      330 TGACAGTGTCTTTCACGACATTCACAGATTGATTCACAGTTACATTAACAGTCTCTTTC 389
Db      1220217 TGGTTGGTGTGTGTGCTTAGATGTCATTTGAGCTTAAGATTGAGTAGC 1220276
QY      390 TACTGTCTGAAAAGAGGCGCTTAAGTGTGTGATTGTGTATTAAGCAATGCAT 449
Db      1220277 GATTAATGTAATGATGTTATTAAGAGAGTGGCAAGATTGCCAAC 1220336
QY      450 TGTGCTGTTCCATTAACGATTGAGATTTGTCACCAACCAATTGGAGAGCGTGAACCTT 509
Db      1220337 AGGAGCTATTBAACAACCTTGAAGAAATATTAAATTAATTAACAAATACAGTAAT 1220396
QY      510 CTTCACAGCTCAAGTGAACCTTTGAACGCTTTAAACTCCGTCGCGCCCTTCAT 569
Db      1220397 ATTAATBAAGCTTACATCTTTATGCAAAATGCAAAATTAATCTTATTTCTATTT 1220456
QY      570 AGTATTT 576
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Db 3503 ATTCATTATTATTATTACTGTAATCAACCATCTGGCTTACTGTAATCTGGCTGTC 3562
Qy 762 TGTTCGAGGAGAACTGCTGGTGTGTTCATTCCTTTTCGTCGTCATGTCCTAT 821
Db 3563 TGCAGTGTTCGCTGCTGTGTAGAGTAATACAGCTTCTCGTCGCTGATGATPAA 3622
Qy 822 GCCATTT 828
Db 3623 GGCATTT 3629

RESULT 9
US-08-961-527-41/c
Sequence 41, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunach
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 9828 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-41

Query Match 2.1%; Score 35; DB 4; Length 9828;
Best Local Similarity 49.2%; Pred. No. 2.5;
Matches 92; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
Qy 642 AAAACATTAATTGAAGTGGCTTGATCAGCATATCCAGCTTAATTCGCTGTGAGACTCC 701
Db 4114 AACGCACTACTTAAAGCTTTTCAAGACCTAATATATGACCTGTCTGATTTGAAAAGAC 4055
Qy 702 TCTTCTGGTCTGCTGAGCAATCAATCTACTCTCTGCTGTAAGCTTTGGCTTCC 761
Db 4054 ATTCCATTAATTAATTTACTGTAATCAACCATCTGGCTTCTACTGTGAATTCGGCTGTC 3995
Qy 762 TGTTCGAGGAACTGCTCGTGTGTGTCATTCCTTTTCGTCGTCATGTGGCTTAT 821
Db 3994 TGCAGTGTTCGCTGCTGTGTAGAGTAATACAGCTGTCCTGTCGCTGATGATPAA 3935
Qy 822 GCCATTT 828
Db 3934 GGCATTT 3928

RESULT 10
US-09-710-279-2485
Sequence 2485, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUS480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2485
LENGTH: 462
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-2485

Query Match 2.1%; Score 34.8; DB 4; Length 462;
Best Local Similarity 50.6%; Pred. No. 0.34;
Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
Qy 865 CATTTCCTGGGGTGTGCAAGAAAGATPAGCGCTATPCCACTGTATGAAGAGAA 924
Db 148 CATATTTATCGCCTGCTGTAAGCAATCAATATATCAAAATTAATTAATTAATTAATTA 207
Qy 925 TATCAATCAAAATTAATTCGTGGCGCGACAATATTTATTAACATTAATTCCTTCACT 984
Db 208 TCTCAATTAAGCTAAGAGTAAGCTAATGATTAATTAAGAAAGAAATTAATTAACACT 267
Qy 985 AGCGTTACAGAAACAGCTTAGTCACATGACCGACATGGAATGTG 1030
Db 268 ATGATTAAGATGCTATATATCTAATTAAGCGACACCGAGATTG 313

RESULT 11
US-09-134-001C-1521
Sequence 1521, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1521
LENGTH: 477
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1521

Query Match 2.1%; Score 34.8; DB 3; Length 477;
Best Local Similarity 50.6%; Pred. No. 0.35;
Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
Qy 865 CATTTCCTGGGGTGTGCAAGAAAGATPAGCGCTATPCCACTGTATGAAGAGAA 924
Db 163 CATATTTATCGCCTGCTGTAAGCAATCAATTAATTAATTAATTAATTAATTAATTAATTA 222
Qy 925 TATCAATCAAAATTAATTCGTGGCGCGACAATATTAATTAACATTAATTCCTTCACT 984

Db 223 TCTCAATTAGACTCAAGAGTAAGACTAATGATTATATAGAAAGAAATTATTAACACT 282
Qy 985 AGCCTTACGAAGACGCTCTAGTCAACATGACCGACGATGAGTGTG 1030
Db 283 ATGATTAAAGATCGTATATACTAATAAGACGACACAGGATTTTG 328

RESULT 12
US-09-710-279-4015/c
Sequence 4015, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4015
LENGTH: 3926
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-4015

Query Match 2.1%; Score 34.8; DB 4; Length 3926;
Best Local Similarity 50.6%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 865 CATTTTCTGGGGGTGCTGCAAGAAAGATAGCGCTATACCACTGTGATGAAGAGGA 924
Db 3455 CATTTTATCCCTGCTGCTGTAAGGCAATCAATATGATTAATTAACGGAACA 3396
Qy 925 TATCAATCAAAATATTTCTGGCTGCGCGCAAAATATTTAATTAACATGAAATCTTCCACT 984
Db 3395 TCTCATATAGACTCAAGAGTAAGACTAATGATTATATAGAAACAGAAATTTATTAACACT 3336
Qy 985 AGCCTTACGAAGACGCTCTAGTCAACATGACCGACGATGAGTGTG 1030
Db 3335 ATGATTAAAGATCGTATATACTAATTAAGACGACACGAGGATTTTG 3290

RESULT 13
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: PALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSES: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9c-Fls
US-08-232-463-14

Query Match 2.1%; Score 34.8; DB 1; Length 7218;
Best Local Similarity 7.6%; Pred. No. 2.4; Indels 0; Gaps 0;
Matches 33; Conservative 203; Mismatches 200; Indels 0; Gaps 0;

Qy 1200 AAAAATGTAATTTTGCATATATAGTGTCTCATTAAGACAGAGGTGTTATTACTTGC 1259
Db 1506 AAAACGGCATGTGAGCATCACTATTAACCTATATCAAGATGTTAAAGATAGA 1447
Qy 1260 CCCAGTGGCAACCTTATCTGTATATGATATATACGATATCACTTTACGAAGACTGA 1319
Db 1446 AGAATTTGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1387
Qy 1320 AGTTCCCTGCTGCAAGTCTGGAAGTGTGATGAGCAACGCTGACCTATTAAGTGG 1379
Db 1386 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1327
Qy 1380 GGATGAGCGTACCTATATCTCTCTTGTGTGCAAGATTTGCTCGGACTTAAGT 1439
Db 1326 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1267
Qy 1440 TAACATTAACATGGCTCCCAAGCAGACAGATGGAAGGACGATCATGTGGAACATAA 1459
Db 1266 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1207
Qy 1500 TGTGATCATGAGCATGCTCAGACATCATAGCTAATCATGACAAAGACCAAGGTTAA 1559
Db 1206 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1147
Qy 1560 GTACATAACCTTTATGAGAAGCTGTGAGACATTCGGGGAAGAAACCGCATGCTGGGA 1619
Db 1146 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1087
Qy 1620 GCTTGATTAAGTGGG 1635
Db 1086 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1071

RESULT 14
US-09-621-976-2813/c
Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 235..399
US-09-621-976-2813

Query Match 2.1%; Score 34.6; DB 4; Length 832;
Best Local Similarity 9.4%; Pred. No. 0.6;

Matches 34; Conservative 164; Mismatches 163; Indels 0; Gaps 0;

QY 960 TATTAACATTGAATTCCTCCACAGGCTTACAGAAACAGCTCAGTCAACATGACACAG 1019
DB 363 TTTTMMKTMWMTTWTTRMMMKKAKRWYMKSTYACASRKRTTGMWMTMMKGM 304
QY 1020 CATGAAATGTGCGCTCCACCCCTTTTGTCTTTCACAGCCCGTGAAGTACAGATGGAGC 1079
DB 303 MSTRWYCMCKKCCMYRGRRCAMYTMAAGRMWSYAMGKMSRMSMSCTMYKKGSTY 244
QY 1080 TCTTTCAAGCAATAGAGACTATGACCCGATAGACAGAGATGTTACACAGTTAA 1139
DB 243 WTMKCTCATWCMYWKYMKRMSKTCWSGSGYMTSYSTRSYSMYASMMYTMCMWVG 184
QY 1140 GAAGTTGATCATGATGACCTGTTTAACTCTGACCTCTGAGAGACCACTAT 1199
DB 183 RWSSTYMWAMGCKMWRATTTWRBAMMMWMAATMMYMWAMCWSRGAAMYRRTMMW 124
QY 1200 AAAAATGATTTTGCATATATGCTCATCTAAAGACAGAGTTGTTATTTACCTTGC 1259
DB 123 GYRYMRKRSYRTRCMAAYAMKTRSYWCMRWKRCMMWMAAYGKTMWRACWK 64
QY 1260 CCCAAGTGGCAACCTTATCTGATATGATGATCATCAGGATTCATTAAGAACTGA 1319
DB 63 TRYRMMWAMMMWMTMMWYMYWRAMKRRMMKRSWMMWMAWGMTWMAABMMWR 4
QY 1320 A 1320
DB 3 W 3

RESULT 15

US-09-389-681-443/C
Sequence 443, Application US/09389681A
Patent No. 6518237
GENERAL INFORMATION:
APPLICANT: Yugui, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangshun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
FILE REFERENCE: 210121.470C3
CURRENT APPLICATION NUMBER: US/09/389,681A
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 443
LENGTH: 511
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(511)
OTHER INFORMATION: n = A,T,C or G
US-09-389-681-443

Query Match 2.1%; Score 34.4; DB 4; Length 511;
Best Local Similarity 46.9%; Pred. No. 0.5;
Matches 107; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 961 ATTAACATTGAATTCCTCCACTAGGCTTACAGAAACAGCTTAGTCAATACACAGC 1020
DB 233 ATGATCTTGGCACTGTCAGACACGAGCAGAGACTAGAACCCCAAGTCAACAGGAACACC 174
QY 1021 ATGAATGTGCGCTTCCACCTTTTGTCTTTCACAGCCCGTGAACCTAGCAGATGGGACT 1080
DB 173 ATCTATAGCACCCCTGCTGCTGTCATGACATTTGTGTCACACACTGCTGTGCTTACATG 114
QY 1081 CTTTCAAGCAATAGAAAGCTATGACCCAGATAGCAAGAGATGTTACACCACTTAAAG 1140
DB 113 CTATTCAAGCCAGCTTAAACCCCTGCTGCTCTCAGAGGGTCTGAGGCAATAGCTGGA 54
QY 1141 AAGTTGATCATGATGACCTGTTTAACTCTGACTGACTCTGAGAG 1188
DB 53 ATGTGATTTAAGTAAAGAAATCGTAGCAATGAGCGAGCCTTGGGGG 6

Search completed: November 8, 2004, 22:59:33
Job time: 162 secs

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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 22:55:47 ; Search time 852 Seconds
(without alignments)
10370.111 Million cell updates/sec

Title: US-09-651-651-4

Perfect score: 1641
Sequence: 1 atggagcgaattcgaattc.....ctgataaagtggtctatcaa 1641

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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19: /cgn2_6/ptodate/1/pubpna/US10F_NEW_PUB.seq:*
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21: /cgn2_6/ptodate/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	591.8	36.1	1719	US-10-437-963-76086	Sequence 76086, A
2	252.6	15.4	1760	US-10-424-599-16008	Sequence 16008, A
3	215.8	13.2	528	US-10-424-599-134518	Sequence 134518, A
4	193	11.8	924	US-10-425-115-137717	Sequence 137717, A
5	187.8	11.4	848	US-10-425-115-93907	Sequence 93907, A
6	173.8	10.6	1383	US-10-425-115-93909	Sequence 93909, A
7	120.8	7.4	1433	US-10-424-599-17331	Sequence 17331, A
8	120.8	7.4	380	US-10-424-599-57573	Sequence 57573, A
9	56.6	3.4	369	US-10-425-115-57116	Sequence 57116, A
10	51	3.1	962	US-10-425-115-61794	Sequence 61794, A
11	44	2.7	374	US-10-425-115-93908	Sequence 93908, A
12	38.8	2.4	486	US-10-465-217-13	Sequence 13, Appl

13	38	2.3	1545	US-10-424-599-56537	Sequence 56537, A
14	37.6	2.3	394	US-10-242-535A-23539	Sequence 23539, A
15	37.6	2.3	394	US-10-085-783A-23539	Sequence 23539, A
16	37.6	2.3	473	US-10-060-036-226	Sequence 226, App
17	37.6	2.3	3737	US-10-240-965-140	Sequence 140, App
18	36.6	2.2	1939	US-10-425-115-31256	Sequence 31256, A
19	36.2	2.2	3325	US-10-437-963-65323	Sequence 65323, A
20	36	2.2	735	US-10-437-963-38267	Sequence 38267, A
21	36	2.2	2395	US-10-437-963-38278	Sequence 38278, A
22	36	2.2	2433	US-10-321-802-21	Sequence 21, Appl
23	35.6	2.2	2356	US-09-822-830A-324	Sequence 324, App
24	35.6	2.2	4089	US-09-764-877-3884	Sequence 3884, App
25	35.6	2.2	4089	US-10-242-515-3884	Sequence 3884, App
26	35.6	2.2	17703	US-10-257-166-34	Sequence 34, Appl
27	35.6	2.2	43680	US-10-257-166-34	Sequence 34, Appl
28	35.4	2.2	160	US-10-242-535A-42853	Sequence 42853, A
29	35.4	2.2	160	US-10-085-783A-42853	Sequence 42853, A
30	35.4	2.2	416	US-10-079-623-57	Sequence 57, Appl
31	35.4	2.2	599	US-10-338-110-117	Sequence 117, App
32	35.4	2.2	1119	US-10-767-701-11611	Sequence 11611, A
33	35.4	2.2	3172	US-10-739-930-1299	Sequence 1299, App
34	35.2	2.1	2456	US-10-437-963-61433	Sequence 61433, A
35	35.2	2.1	7219	US-10-437-963-13743	Sequence 13743, A
36	35	2.1	9828	US-08-961-527-41	Sequence 41, Appl
37	35	2.1	9828	US-10-158-844-41	Sequence 41, Appl
38	35	2.1	2256646	US-10-470-565-1	Sequence 1, Appl1
39	34.8	2.1	507	US-10-282-122A-10934	Sequence 10934, A
40	34.8	2.1	560	US-10-125-668-962	Sequence 962, App
41	34.8	2.1	8711	US-10-221-714A-424	Sequence 424, App
42	34.6	2.1	916	US-10-184-634-78	Sequence 78, Appl
43	34.6	2.1	916	US-10-184-634-78	Sequence 78, Appl
44	34.6	2.1	26112	US-09-764-872-627	Sequence 627, App
45	34.4	2.1	511	US-09-604-287A-443	Sequence 443, App

ALIGNMENTS

RESULT 1
US-10-437-963-76086
; Sequence 76086, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 76086
; LENGTH: 1719
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_76111C.1
; US-10-437-963-76086

Query Match 36.1%; Score 591.8; DB 17; Length 1719;
Best Local Similarity 65.2%; Pred. No. 9.2e-174;
Matches 1029; Conservative 0; Mismatches 382; Indels 166; Gaps 4;

QY 108 CGACTCTCGAAGCTATGCGGTATATATCTTCGCGGATTTCCGTCGACGACGCTACAGC 167
DB 123 CGACTCTCGAAGCTATGCGGTATATATCTTCGCGGATTTCCGTCGACGACGCTACAGC 182

OY	168	TTGTGTCGATCCCTTGA	CTGTCCATTAAC	TCCTGGT	TGACATTC	CGCTGAC	CTTCGAT	GC	227
Db	183	GTGGTCTGTGTG	CGATATGGCCCT	CTACG	CCCTTGAC	CTTCAAC	CCCCCT	CGACT	242
OY	228	GCTAAGACAC	ACTAAGCTTCTTCT	CTGCTG	TCMACTG	CTGGTGT	TAAGTGA	TGATG	287
Db	243	GCTGACAC	CCGCCAAGCTCTTAT	CTGTCTGT	CAATTG	CTGTGCT	CAAAATG	CAATG	302
OY	288	TCCTTATAT	CAACAGACCAAT	CCCGAG	TGAAGT	CACGG	CTGACAG	TGGTCTT	347
Db	303	CCCTTACA	CAACGAGATCAT	CCAGAG	TCMAAGT	CAAGG	CTGACAG	TGGTCTT	362
OY	348	CATCA	CAGAAATTTG	GATCCAG	GTTCATATA	CAGTCTCTT	CTACTGT	CTGGAAG	407
Db	363	AATTAC	AGATTAGACCC	CTGTATATATA	CTGTGCTCTT	CTTCTT	CAGTGTG	GAAGAA	422
OY	408	GCTTA	GTTGTGTGTG	ATTGATTG	TAGAA	CAATATG	CAATTTG	CGCTGT	467
Db	423	GGTCAAA	TG-----						431
OY	468	TTGAG	ATTGTTCACCA	CCAAATTTG	GAAGCG	TGACCTT	ATCAAG	CTCAAGT	527
Db	432	-----							434
OY	528	GACCTT	GAAACTGCTTT	AAAACT	CCGTG	CGGCGCCCTT	CTATAG	TAATTTGG	587
Db	435	AACTTT	GAAATG	CAATG	AAATTC	CGAGAG	GGGCTCTT	TAAGTGT	494
OY	588	GGGTAA	TATATGTCTT	CAGAT	ACTTCTG	GAATGG	CTGAG	GGCTAG	647
Db	495	GGGTAA	TATATGTCTT	CGCTACTT	CTGGAAT	TGTTGA	AACTAG	AAATCGCT	554
OY	648	TTATTT	GAAAGTG	CTTGA	TACAG	ATATCCAT	TATTCG	CTGTG	707
Db	555	TTACAT	CCGATGG	CTTGA	CGAACAT	ATATCAT	ATCTT	GTGAG	614
OY	708	TGTTCT	GTGGA	GGCAAT	CAATCT	ACTCTCT	CTGTG	TAACTT	767
Db	615	TGTTCT	GTGGA	GGCAAT	CAATCT	ACTCTCT	CTGTG	TAACTT	767
OY	768	TGAGG	GAATCTG	TCGGT	TGTGCA	ATCTTTC	CGTCA	TGTG	827
Db	675	CGAGG	GAATCTG	TCGGT	TGTGCA	ATCTTTC	CGTCA	TGTG	827
OY	828	TTCA	AAGATTG	CAAGG	GTATAC	ATCACT	CTGGA	CGATTTT	887
Db	735	CTC	AGAAATTTG	CAAGG	GTATAC	ATCACT	CTGGA	CGATTTT	887
OY	888	GAA	AGATAAG	CGGTA	TATCA	CTGTG	ATG	AAGAA	947
Db	793	-G	TTGCC	CAACCA	GACAG	ATGTGA	TGAATA	TGAAT	851
OY	948	GCGG	CAAAATAT	TATTA	CATTG	AAATTC	CTTCC	ATAG	1007
Db	852	GCGG	CAAAATAT	TATTA	CATTG	AAATTC	CTTCC	ATAG	1007
OY	1008	CA	CAATG-----						1048
Db	912	CATT	ATGATAC	ATC	ATG	AAATAT	CAAT	CAAT	971
OY	1047	GTCTT	TCACAG	CCGCT	GAACT	AGATG	GAATCT	TTTCA	1106
Db	972	GTCA	TTTTCTGT	AGGAG	GTTCAG	ATGTG	TAATCT	GTTTAA	1031
OY	1107	CCCA	ATATG	CAAGAG	ATG	TATAC	CAAG	ATG	1167
Db	1032	CCCT	CAAGAG	ATG	ATG	TATAC	CAAG	ATG	1091
OY	1167	TAA	TCTCTG	ATC	CTG	TGGA	GAG	CAAC	1228
Db	1092	TAA	TCTCTCT	CA	CCCTG	GAAG	AGAC	CCCA	1151
OY	1227	TCAT	CTAA	AGAC	AG	GTGTG	TTATCTT	TG	1286

[illegible]

Db 256 TTCTGCTGCAAAAACGCTGTGACCGAAAGTAAACAAAGCTCCACAGTCAGA 315
Oy 1467 ACACGATGAGACGACGATGATGTAATGTTGATGATGATGATGATGATGATGAT 1526
Db 316 GCATGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 375
Oy 1527 CATAGCTAACATGACAAAGACCAAGGATTAAGTACATTAACCTTTATGAAGACTGTA 1586
Db 376 CGTTCCAAACATGACAGATCACCAGGATGATGATGATGATGATGATGATGATGAT 435
Oy 1587 GAGCATTCGGGGAAGAGAACCCGATCTGGAGCTTATATAA 1629
Db 436 AAGTCTTCTGGAAGAGACAGAGCTTTGGAGCTTATATAA 478

RESULT 3

US-10-424-599-134518
; Sequence 134518, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 134518
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_9247C.1
US-10-424-599-134518

Query Match 13.2%; Score 215.8; DB 16; Length 528;
Best Local Similarity 80.7%; Pred. No. 2.6e-56;
Matches 264; Conservative 0; Mismatches 62; Indels 1; Gaps 1;

Oy 108 CGACTACTCGAAGCTATCGGATATATATATATATATATATATATATATATATATAT 167
Db 202 CGACTACTCGAAGCTATCGGATATATATATATATATATATATATATATATATATAT 261
Oy 168 GTGCTGATCTTGAATCTGATATATATATATATATATATATATATATATATATAT 227
Db 262 ATGCTGATCTTGAATCTGATATATATATATATATATATATATATATATATATAT 321
Oy 228 GCTGACACCACTAAGCTTCTTCTGCTGATATATATATATATATATATATATATATAT 287
Db 322 GCTGACACCACTAAGCTTCTTCTGCTGATATATATATATATATATATATATATATAT 381
Oy 288 TCCTTATATATCAACAGACATCCGAGTATATATATATATATATATATATATATATAT 347
Db 382 TCCTTATATCAACAGACATCCGAGTATATATATATATATATATATATATATATATAT 441
Oy 348 CATCAACGAATTTGATTCAGGTTATATATATATATATATATATATATATATATATAT 406
Db 442 CATTAACGAATTTGATTCAGGTTATATATATATATATATATATATATATATATATAT 501
Oy 407 GGCTTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 433
Db 502 GGATTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 528

RESULT 4

US-10-425-115-137717
; Sequence 137717, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 137717
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_57075C.1
US-10-425-115-137717

Query Match 11.8%; Score 193; DB 18; Length 924;
Best Local Similarity 79.2%; Pred. No. 5.1e-49;
Matches 229; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Oy 239 CTAGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 298
Db 590 CTGCTCTTCTCTGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 649
Oy 299 AAGACACATCCGAGTATATATATATATATATATATATATATATATATATATATATAT 358
Db 650 AGATAGACATCCGAGTATATATATATATATATATATATATATATATATATATATATAT 709
Oy 359 TGATTCAGGTTATATATATATATATATATATATATATATATATATATATATATATAT 418
Db 710 TGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769
Oy 419 GTGTTGATTTGATATATATATATATATATATATATATATATATATATATATATATAT 478
Db 770 GTGTTGATTTGATATATATATATATATATATATATATATATATATATATATATATAT 829
Oy 479 CACCAACCAATTTGAGAGGCTGACCTTTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 527
Db 830 CCCATCAATGCTTGAAGAGAGATCTGATCTTTCACCAATTAAGTT 878

RESULT 5

US-10-425-115-93907
; Sequence 93907, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 93907
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_18630C.1
US-10-425-115-93907

Query Match 11.4%; Score 187.8; DB 18; Length 848;
Best Local Similarity 77.3%; Pred. No. 2.1e-47;
Matches 228; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Oy 246 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
Db 387 TTTCTGCGGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 446

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Qy 306 CCATCCGAGGTGTAAGTACAGCCCTGACAGTGTCTTTACGCCATCAGAAATGGATCC 365
Db 447 CCATCCGAGGTGTAAGTACAGCCCTGACAGTGTCTTTACGCCATCAGAAATGGATCC 506
Qy 366 AGTTACATACAGGCTCTTTCTTCTACAGTGTGGAAGAGTGGCTTAAGTGGTGTGA 425
Db 507 TGGTTATATACAGGCTCTTTCTTCTACAGTGTGGAAGAGTGGCTTAAGTGGTGTGA 566
Qy 426 GTTGTGATAGAGCAAAATGCAATTTGCTGCTTTCCATACGATTTGGAGATTTGCAAC 485
Db 567 GTTGTGATAGAGCAAAATGCAATTTGCTGCTTTCCATACGATTTGGAGATTTGCAAC 626
Qy 486 CAAATTGGAAGAGCTGACCTTTACTTTCACAGCTCAAGTTGACCTTTGAACT 540
Db 627 AATGCTTGAGAGAGAGATCTGTACTTTCACAAATTAACAGATCAAGTAAGAT 691

RESULT 6
US-10-425-115-93909
; Sequence 93909, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 93909
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_185632C.1
US-10-425-115-93909
```

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Query Match 10.6%; Score 173.8; DB 18; Length 1383;
Best Local Similarity 76.8%; Pred. No. 6.8e-43;
Matches 228; Conservative 0; Mismatches 62; Indels 7; Gaps 1;

Qy 238 ACTAAGCTTCTTCTGCTGTCAGACTGCTGTTAAGTATGCTGATGCTTATAT 297
Db 696 ACATGCTTTCTCTGACGTAATATGCTGCTTAATGATGCTGCTGAACCTATAT 755
Qy 238 CAAACAGACATCCCGAGTGAAGTACAGGCTGACAGTGTCTTTGACCATCAGAA 357
Db 756 CAGACAGACATCCCGAGTGAAGTGAAGTGAAGTGTGCTTTCTGCAATTACAGAG 815
Qy 358 TTGATTCAGGTTACATA-----CAGGTCTCTTTCTCTGCTGCTGGAAGAGTGGCT 410
Db 816 CTGACCTGCTTATATACAGGTTCAAGTCTCTCTCTTCAAGTATGGAAGATGGCT 875
Qy 411 TAAAGTGTGTGTTGATTTGATGAAGCAATGCAATGCTGCTGTTCCATGATG 470
Db 876 CAAATGCTGTGAAGTGTGGATGAAGTGAATGCAATTCGCTGTTCCGATGATG 935
Qy 471 GAGATTTCACCAACCAAAATGGAAGAGCTGACCTTTACTTTCAAGCTCAAGTT 527
Db 936 GAGACTGCCCCATCAATGCTTGAGAGAGAGATCTGTACTTTCACAAATTAAGTT 992
```

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RESULT 7
US-10-424-599-17331
; Sequence 17331, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
```

```
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 17331
; LENGTH: 1433
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1433)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_115655C.1
US-10-424-599-17331
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Query Match 7.4%; Score 120.8; DB 16; Length 1433;
Best Local Similarity 70.5%; Pred. No. 2.8e-26;
Matches 186; Conservative 0; Mismatches 57; Indels 21; Gaps 1;

Qy 903 ATACCTGATGATGAGAGGAATATCAATCAAAATATTGCTGGCGCGCAAAATATAT 962
Db 49 ATACCTGATGATGAGAGGAATATCAATCAAAATATTGCTGGCGCGCAAAATATAT 108
Qy 963 TAACTTGAATTTCTTCACTACG-----TTACAGAAACAGC 1001
Db 109 CAATTTGAATTTCTTCACTACG-----TTACAGAAATATAC 168
Qy 1002 TCTATGATGATGACGAGATGATGATGCTTCCACCTTTGCTTTCAACAGCCG 1061
Db 169 TGAAGCCAACTTGTCCAGATGAGTGGAGCTACTCAATTAATCTTCTGAGCTCG 228
Qy 1062 TGAATGAGAGAGAGAGCTTTTCAAGCAATGAAAGATGATGACGAGATGAGAG 1121
Db 229 GGAATATGAGATGAGAGCTTTTCAAGCAATGAAAGATGATGACGAGATGAGAG 288
Qy 1122 GATGTTACACCAATTAAAGAGTT 1145
Db 289 GCTCTTGTACTGTTAGAGAGTT 312
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```
RESULT 8
US-10-424-599-57573
; Sequence 57573, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 57573
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_22C.1
US-10-424-599-57573
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Query Match 4.4%; Score 72.2; DB 16; Length 380;
Best Local Similarity 61.2%; Pred. No. 2e-11;
Matches 167; Conservative 0; Mismatches 103; Indels 3; Gaps 3;

Qy 1234 AAGCAGAGGTGTTATTTCTTTGCTTCCCAAGTGGCAAACTTATCTGATTAATTGATC 1293
```

Db 109 AAGAAATAGACGGTAAGTAAGTCTAGCCGTGAGCCCTTACCTGAACTGATGATC 168
Qy 1294 ATCAAGGATATCAT-TTACGAAACTGAAAGTTCCCTGCTGATCAAGTCTGGAAGTGTG 1352
Db 169 ATTACTGTGGCGCATTCAGATAGCGTAGCGCAGATGTCTTGTGATCAGACAAAGAAATCCG 228
Qy 1353 TGATGGAAACCGCTGACCTATTAAGTGGAGATGAGACGGTACCTATTCATCTCTCTTG 1412
Db 229 TGGAGGGAACCTGTATCATATGC-CGGCATGAGACGGCGCATATCTTATCCCTTTCTG 287
Qy 1413 GTGCAAGATTTGCTCGGACCTTAAGTTAACATA-ACATAGTCTCCCAAGCAGAACAG 1471
Db 288 GAGCAGAAACAGCGCTTGTCTCCGATGTCACATATACCAAGCCCACTGTGTAGCAGC 347
Qy 1472 ATGGAAGGACGATCATGTGAACTAAATGTTG 1504
Db 348 AAGGTCAGATGTTTCACTTAATTGATGTGG 380

RESULT 9
US-10-425-115-57116
; Sequence 57116, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 57116
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(369)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_152078C.1
US-10-425-115-57116

Query Match 3.4%; Score 56.6; DB 18; Length 369;
Best Local Similarity 78.2%; Pred. No. 1.5e-06;
Matches 68; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 238 ACTAAGCTTTCTTGGCTGCTCACTGCTTTAAGTGTAGTGGCTGATCCTTATAT 297
Db 283 ACATTGCTTTCTGCAAGTAATGCTGGCTTAATGATGCTGTAACCTTATAT 342
Qy 298 CAAACAGACATCCCGAGTGTAGTCA 324
Db 343 CAGATAGCATCCCGAATGCAAGTCA 369

RESULT 10
US-10-425-115-61794
; Sequence 61794, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 61794
; LENGTH: 962
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_15634C.1
US-10-425-115-61794

Query Match 3.1%; Score 51; DB 18; Length 962;
Best Local Similarity 80.0%; Pred. No. 0.00016;
Matches 60; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1555 GTTAAGTACATTAACCTTTTATGAAGACTGTGAGACATTTCCGGGAAAGAACCGGACTC 1614
Db 32 GTGAAGTACATTAACCTTACTATGAGAGATGTGAAAGTCTTCAGAGATGGAAGAACGACTC 91
Qy 1615 TGGAGCTGTATATA 1629
Db 92 TGGAGCTCGATATA 106

RESULT 11
US-10-425-115-93908
; Sequence 93908, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 93908
; LENGTH: 374
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(374)
; OTHER INFORMATION: Clone ID: MRT4577_185631C.1
US-10-425-115-93908

Query Match 2.7%; Score 44; DB 18; Length 374;
Best Local Similarity 83.3%; Pred. No. 0.013;
Matches 50; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 321 GTCAAGGCTGACAGTGTGCTTTTCAGCCATCAGAGAAATGGATCCAGTTACATACAG 380
Db 1 GTCAAGGCTGATAGTGTGCTTTTCGCAATTACAGAGCTGAGCCCTGTTATATACAG 60

RESULT 12
US-10-465-217-13/C
; Sequence 13, Application US/10465217
; Publication No. US20030204859A1
; GENERAL INFORMATION:
; APPLICANT: Kazemi-Bsfarjani, Parsa
; APPLICANT: Benzer, Seymour
; TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE
; TITLE OF INVENTION: TOXICITY, METHODS OF USE, AND MODULATORS OF POLYGLUTAMINE
; TITLE OF INVENTION: TOXICITY
; FILE REFERENCE: 06618-68601
; CURRENT APPLICATION NUMBER: US/10/465,217
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US/09/639,207
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: US 60/148,934
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: US 60/148,933
; PRIOR FILING DATE: 1999-08-12

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1 PRIOR APPLICATION NUMBER: US 60/177,047
2 PRIOR FILING DATE: 2000-01-18
3 PRIOR APPLICATION NUMBER: US 60/205,720
4 PRIOR FILING DATE: 2000-05-19
5 NUMBER OF SEQ ID NOS: 69
6 SOFTWARE: Fastseq for Windows Version 4.0
7 SEQ ID NO 13
8 LENGTH: 486
9 TYPE: DNA
10 ORGANISM: Artificial Sequence
11 FEATURE:
12 OTHER INFORMATION: Synthetic DNA
13 US-10-465-217-13

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Query Match	2.4%	Score 38.8;	DB 15;	Length 486;
Best Local Similarity	56.2%;	Pred. No. 0.67;		
Matches 73; Conservative	0;	Mismatches 57;	Indels 0;	Gaps 0;

Oy 662 TTATCATGCAATATCCATGCTATATTCGGCTGTGAAGCTCTCTCTTGATGTTCTGTAGG 721
 Db 183 TTGTGCTGCTGTGTGCTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 124
 Oy 722 CAATCAAAATATCTCTCTCGGTGAAGCTTGGGCTTCCTGTTTCTGAGGAAGCTGCTC 781
 Db 123 CTGTGTGCTGCTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 64
 Oy 782 GGTGTGTTGTC 791
 Db 63 GGGGGTTGAC 54

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RESULT 13
US-10-424-599-56537
Sequence 56537, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 56537
LENGTH: 1545
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_22062C.1
US-10-424-599-56537

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Query Match	2.3%	Score 38;	DB 16;	Length 1545;
Best Local Similarity	53.3%	Pred. No. 2.5;		
Matches	80;	Conservative	0;	Mismatches 70;
			Indels	0;
			Gaps	0;

QY	565	TCCTATAGATTTGGCCATTCATGGGTATATAGCTTCAGATATCTTCTGGATAGGCTG	624
Db	956	TCCTATTTTGGGTGCAACAGTGGTTAGATATCTTAATVACTTGGGACAAATAGCTG	1015
QY	625	AGGCTAGAAATTCGCCAAATCATTTTGGAGTGGCTTGATACGATATCATGCTTAT	684
Db	1016	AATCCAGGGGTGGCTCTAATATTTATCTTTGGGTCTTTGGTCATCATCGTTGGGTCT	1075
QY	685	TTGCGTGTGGAGCTCCTCTCTCTGGTTCCT	714
Db	1076	TTGGCGGTCTCATGCGCATCTCTTATAGTACT	1105

RESULT 14
US-10-242-535A-23539

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Sequence 23539, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Hiew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23539
LENGTH: 394

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Query Match	2.3%	Score 37.6	DB 16	Length 394
Best Local Similarity	57.8%	Pred. No. 1.4		
Matches 67; Conservative	0	Mismatches 49	Indels 0	Gaps 0

Oy 998 CAGGTCTAGTCACATGATACACGAGATGGAAATGGCCCTTCCACCCCTTTTGCTTTCAAG 1057
 124 CAGGAGTTCTGAAATGTGAGCATCTCGCAAGAAATGTTGACACCATATATATGCTTTCCAC 183
 Oy 1058 CCCGTGAATACGACGATGGGAACTCTTTTCAAGCAATATGAAAGACTATGACCCCAAGT 1113
 184 ACTTTTACCAAGACGATGAGAGGTTTGTCTTCTGCATATGAAAGGATGACACCCCAAT 239

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RESULT 15
US-10-085-783A-21539
Sequence 23539, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12

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/ PRIOR APPLICATION NUMBER: US 60/271,955
/ PRIOR FILING DATE: 2001-02-28
/ NUMBER OF SEQ ID NOS: 58994
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 23539
/ LENGTH: 394
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (55)..(55)
/ OTHER INFORMATION: n 1s a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (89)..(89)
/ OTHER INFORMATION: n 1s a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (348)..(348)
/ OTHER INFORMATION: n 1s a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (384)..(384)
/ OTHER INFORMATION: n 1s a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (389)..(389)
/ OTHER INFORMATION: n 1s a, c, g, or t
/ OTHER INFORMATION: n 1s a, c, g, or t
US-10-085-783A-23539

Query Match      2.3%; Score 37.6; DB 16; Length 394;
Best Local Similarity 57.8%; Pred. No. 1.4;
Matches 67; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 998 CAGCTCTAGTCAACATGACCGCATGAGATGCGCTTCCACCCCTTTGTCTTTCACAG 1057
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 CAGAGTTCTGAAATGTCAGCATCTGCAGAAATGTCACCCATCATTTATGTTTCCAC 183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 1058 CCCGTGAAGTGAAGATGGAGCTTTTCAAGCAATAGAGACTATGACCCAGAT 1113
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 ACTTTTACCAAGCAGATGAGAGGTTTCTTCTGCCATGAGAGCATGCACCCAAT 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: November 9, 2004, 02:42:43
Job time : 856 secs

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OM nucleic - nucleic search, using bw model

Run on: November 9, 2004, 00:29:47 ; Search time 836 Seconds
(without alignments)
10304.187 Million cell updates/sec

Title: US-09-651-651-4
Perfect score: 1641
Sequence: 1 atcgagagcgaatcgaatc.....ctgataaagctgggtatctaa 1641

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 413486 seqs, 2624710521 residues

Word size : 0
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_23Sep04:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1641	100.0	1641	5 AAS01082	AAS01082 Arabidops
2	1375	83.8	1902	12 ADF47823	ADF47823 Arabidops
3	243	14.8	3896	3 AAC64438	AAC64438 Arabidops
4	183	11.2	3896	3 AAC64448	AAC64448 Arabidops
5	27	1.6	44	5 AAS01322	AAS01322 Arabidops
6	26	1.6	40	5 AAS01323	AAS01323 Arabidops
7	20	1.2	31140	4 ABA06791	ABA06791 Human rep
8	20	1.2	31140	4 ABA08065	ABA08065 Human cva
9	20	1.2	226475	9 AAD58279	AAD58279 Human tum
10	19	1.2	407	3 AAA42733	AAA42733 Human sec
11	19	1.2	453	4 ABA08624	ABA08624 Human sec
12	19	1.2	453	10 ADC32511	ADC32511 Human nov
13	19	1.2	909	3 AAC76568	AAC76568 Human ORF
14	19	1.2	1468	10 ADC30740	ADC30740 Human nov
15	19	1.2	1584	8 ACA21590	ACA21590 Prokaryot
16	19	1.2	2340	12 ADM72574	ADM72574 Nucleotid
17	19	1.2	2372	12 ADM72577	ADM72577 Nucleotid
18	19	1.2	2372	12 ADM72581	ADM72581 Nucleotid
19	19	1.2	2372	12 ADM72585	ADM72585 Nucleotid
20	19	1.2	2372	12 ADM72587	ADM72587 Nucleotid
21	19	1.2	2372	12 ADM72589	ADM72589 Nucleotid

C 22	19	1.2	2372	12	ADM72572	ADM72572 Nucleotid
C 23	19	1.2	2372	12	ADM72586	ADM72586 Nucleotid
C 24	19	1.2	2372	12	ADM72590	ADM72590 Nucleotid
C 25	19	1.2	2372	12	ADM72575	ADM72575 Nucleotid
C 26	19	1.2	2372	12	ADM72581	ADM72581 Nucleotid
C 27	19	1.2	2372	12	ADM72576	ADM72576 Nucleotid
C 28	19	1.2	2372	12	ADM72583	ADM72583 Nucleotid
C 29	19	1.2	2372	12	ADM72588	ADM72588 Nucleotid
C 30	19	1.2	2372	12	ADM72573	ADM72573 Nucleotid
C 31	19	1.2	2372	12	ADM72578	ADM72578 Nucleotid
C 32	19	1.2	2372	12	ADM72580	ADM72580 Nucleotid
C 33	19	1.2	2372	12	ADM72582	ADM72582 Nucleotid
C 34	19	1.2	2372	12	ADM72584	ADM72584 Nucleotid
C 35	19	1.2	2372	12	ADM72592	ADM72592 Nucleotid
C 36	19	1.2	2372	12	ADM72597	ADM72597 Nucleotid
C 37	19	1.2	2488	2	AAV74418	AAV74418 Staphyloc
C 38	19	1.2	5331	4	AAK83051	AAK83051 Human imm
C 39	19	1.2	7022	4	AAK83051	AAK83051 Human imm
C 40	19	1.2	8495	10	ADC30133	ADC30133 Human nov
C 41	19	1.2	13309	4	AAK83980	AAK83980 Human imm
C 42	19	1.2	172637	6	ABN83124	ABN83124 Human vol
C 43	19	1.2	237961	6	ABO80552	ABO80552 Human Can
C 44	18	1.1	125	3	AAC12300	AAC12300 Human sec
C 45	18	1.1	153	3	AAC19008	AAC19008 Human sec
C 46	18	1.1	186	6	ABN90933	ABN90933 Staphyloc
C 47	18	1.1	241	4	AAFI7883	AAFI7883 Human bre
C 48	18	1.1	241	4	AAAF7313	AAAF7313 Human bre
C 49	18	1.1	241	6	ABSE63914	ABSE63914 Human bre
C 50	18	1.1	241	10	ABRT33126	ABRT33126 Human tum
C 51	18	1.1	241	11	ADJ93033	ADJ93033 Human bre
C 52	18	1.1	241	12	ADBA4333	ADBA4333 Human cDN
C 53	18	1.1	300	3	AAA00940	AAA00940 Human col
C 54	18	1.1	309	5	ACF71748	ACF71748 Phototrab
C 55	18	1.1	411	10	AAE66394	AAE66394 Novel hum
C 56	18	1.1	451	3	AAC66021	AAC66021 Human lun
C 57	18	1.1	451	6	ABL49240	ABL49240 Human lun
C 58	18	1.1	451	6	ABQ92426	ABQ92426 Human lun
C 59	18	1.1	451	9	ADA28415	ADA28415 Human lun
C 60	18	1.1	451	10	ADH36979	ADH36979 Human lun
C 61	18	1.1	451	12	ADM56782	ADM56782 Human lun
C 62	18	1.1	458	4	AAH55550	AAH55550 Human bre
C 63	18	1.1	458	12	ADN40320	ADN40320 Human bre
C 64	18	1.1	489	3	AAC23414	AAC23414 Human sec
C 65	18	1.1	516	6	ABK44558	ABK44558 cDNA enco
C 66	18	1.1	545	6	ABV87927	ABV87927 Human col
C 67	18	1.1	578	5	ABV53961	ABV53961 Human pro
C 68	18	1.1	738	10	ACF68308	ACF68308 Phototrab
C 69	18	1.1	784	5	AAE82779	AAE82779 DNA enco
C 70	18	1.1	792	6	ABZ13450	ABZ13450 Arabidops
C 71	18	1.1	792	8	ADG88173	ADG88173 A. thalia
C 72	18	1.1	792	8	ADA68169	ADA68169 Arabidops
C 73	18	1.1	889	3	AAC33097	AAC33097 Arabidops
C 74	18	1.1	912	2	AAI03477	AAI03477 Transcrip
C 75	18	1.1	912	3	AAC32847	AAC32847 Arabidops
C 76	18	1.1	920	3	AAC50553	AAC50553 Arabidops
C 77	18	1.1	1024	6	ABX66911	ABX66911 Helicobac
C 78	18	1.1	1232	5	ADQ99002	ADQ99002 Human pol
C 79	18	1.1	1232	5	ADB48762	ADB48762 Novel hum
C 80	18	1.1	1232	9	ADB48762	ADB48762 Novel hum
C 81	18	1.1	1422	8	AAAF7124	AAAF7124 C. glutam
C 82	18	1.1	1539	4	AAAF7124	AAAF7124 C. glutam
C 83	18	1.1	1543	5	AAH14307	AAH14307 H. pylori
C 84	18	1.1	1554	5	AAH66546	AAH66546 C. glutami
C 85	18	1.1	1603	9	ACC59460	ACC59460 C. glutami
C 86	18	1.1	1653	3	AAAC1704	AAAC1704 Arabidops
C 87	18	1.1	1747	2	AAZ24893	AAZ24893 Human sec
C 88	18	1.1	1747	8	ADA40096	ADA40096 Human sec
C 89	18	1.1	1747	8	ACC50600	ACC50600 Human sec
C 90	18	1.1	1747	10	ADCT3671	ADCT3671 Human sec
C 91	18	1.1	1747	10	ADA56270	ADA56270 Gene enco
C 92	18	1.1	1748	10	ADB58615	ADB58615 Toxicity-
C 93	18	1.1	1748	10	ADB53263	ADB53263 Primary r
C 94	18	1.1	1947	2	AAK61429	AAK61429 DNA enco

95	18	1.1	2209	4	AAH19237	AaH19237 Human sec	c 168	17	1.0	200	10	ADC71569	AdC71569 SPC6-spec
96	18	1.1	2304	6	AAZ66863	AaZ66863 Arabidops	c 169	17	1.0	201	2	AAH85669	AaH85669 Human sin
97	18	1.1	2352	3	AAAC5196	AaC5196 Arabidops	c 170	17	1.0	202	2	AAH85669	AaH85669 Human sin
c 98	18	1.1	2414	4	AAH14270	AaH14270 Human cDN	c 171	17	1.0	203	7	AAH85669	AaH85669 Human sin
c 99	18	1.1	2414	8	AAAC50994	AaC50994 Human bla	c 172	17	1.0	204	6	ABL38186	AbL38186 Human col
c 100	18	1.1	2414	12	ADN04937	AdN04937 Antiporci	c 173	17	1.0	205	10	ABX87779	AbX87779 Corn ear-
c 101	18	1.1	2459	4	AAI60568	AaI60568 Human pol	c 174	17	1.0	206	5	ADL40011	AdL40011 Human ova
c 102	18	1.1	2509	4	AAAF62693	AaF62693 Arabidops	c 175	17	1.0	207	2	AAZ13059	AaZ13059 Human gen
c 103	18	1.1	2501	5	AAH82714	AaH82714 DNA encod	c 176	17	1.0	208	300	AAZ17785	AaZ17785 Human gen
c 104	18	1.1	2741	2	AAH86143	AaH86143 DNA encod	c 177	17	1.0	209	10	ADC75311	AdC75311 T harzian
c 105	18	1.1	3238	10	AAK52242	AaK52242 Human pol	c 178	17	1.0	210	321	AAH83348	AaH83348 Enterococ
c 106	18	1.1	3268	2	ADFF6738	AdF6738 Novel hum	c 179	17	1.0	211	6	ABN25879	AbN25879 Human ORF
c 107	18	1.1	3278	2	AAAT62358	AaT62358 Klyverom	c 180	17	1.0	212	3	ABN25879	AbN25879 Human ORF
c 108	18	1.1	3278	2	AAAT72385	AaT72385 K. lactis	c 181	17	1.0	213	5	AD174714	AdI74714 Human ova
c 109	18	1.1	3459	8	AAZ23708	AaZ3708 Human col	c 182	17	1.0	214	8	ABX46449	AbX46449 Bovine ES
c 110	18	1.1	3521	8	AAZ57791	AaZ57791 5' upstre	c 183	17	1.0	215	6	ABL62801	AbL62801 Breast ca
c 111	18	1.1	3582	8	AAFC39318	AaF39318 Mycobacte	c 184	17	1.0	216	4	ABL62801	AbL62801 Breast ca
c 112	18	1.1	3887	4	AAH14236	AaH14236 Human cDN	c 185	17	1.0	217	6	ABN19298	AbN19298 Human ORF
c 113	18	1.1	3887	12	ADOL8922	AdL8922 Human cod	c 186	17	1.0	218	8	ABZ18618	AbZ18618 Human ova
c 114	18	1.1	4027	6	AAO99318	AaO99318 Human cod	c 187	17	1.0	219	5	AD174714	AdI74714 Human ova
c 115	18	1.1	4382	9	AAO80410	AaO80410 AAV9 rep	c 188	17	1.0	220	4	AAI85462	AaI85462 Human imm
c 116	18	1.1	4385	10	AADE76506	AaD76506 Adeno-ss	c 189	17	1.0	221	4	AAK65366	AaK65366 Human imm
c 117	18	1.1	4470	10	ADH28791	AdH28791 Human chr	c 190	17	1.0	222	5	ABAI9054	AbAI9054 Human neu
c 118	18	1.1	4470	12	ADP13530	AdP13530 Renal cel	c 191	17	1.0	223	9	ACH19034	AcH19034 Human adu
c 119	18	1.1	4509	4	AAI60167	AaI60167 Human pol	c 192	17	1.0	224	12	ACH70447	Ach70447 Human gen
c 120	18	1.1	4586	4	AAI58642	AaI58642 Human pol	c 193	17	1.0	225	6	ABQ20867	AbQ20867 Oligonuc
c 121	18	1.1	4586	5	AAO98860	AaO98860 DNA encod	c 194	17	1.0	226	6	ABQ20866	AbQ20866 Oligonuc
c 122	18	1.1	4586	3	ADB48620	AdB48620 Novel unm	c 195	17	1.0	227	6	ABO19486	AbO19486 Oligonuc
c 123	18	1.1	4684	3	AAA62904	AaA62904 Murine jn	c 196	17	1.0	228	6	ABO19487	AbO19487 Oligonuc
c 124	18	1.1	4820	4	AAI60428	AaI60428 Human pol	c 197	17	1.0	229	5	AAH12238	AaH12238 Human cDN
c 125	18	1.1	5425	5	AAAS82780	AaA82780 DNA encod	c 198	17	1.0	230	8	ABX98493	AbX98493 Rice albu
c 126	18	1.1	5473	4	AAI58381	AaI58381 Human pol	c 199	17	1.0	231	4	AAH10604	AaH10604 Human cDN
c 127	18	1.1	5473	5	AAO98590	AaO98590 DNA encod	c 200	17	1.0	232	4	ABAI1179	AbAI1179 Human foe
c 128	18	1.1	5473	9	ADB48350	AdB48350 Novel hum	c 201	17	1.0	233	4	AAI41079	AaI41079 Probe #97
c 129	18	1.1	5581	10	AADE54007	AaD54007 Human pro	c 202	17	1.0	234	4	AAK35366	AaK35366 Human bna
c 130	18	1.1	6412	4	ABLI9284	AbI9284 Drosophil	c 203	17	1.0	235	4	AAK09474	AaK09474 Human hor
c 131	18	1.1	6450	10	ABZ23178	AbZ23178 Polynucle	c 204	17	1.0	236	4	ABSS3104	AbS3104 Human liv
c 132	18	1.1	6450	12	ADN36880	AdN36880 P200 nucl	c 205	17	1.0	237	5	ABZ51545	AbZ51545 Aspergill
c 133	18	1.1	6539	10	AADE57349	AaD57349 Human gen	c 206	17	1.0	238	5	ADL45825	AdL45825 Human ova
c 134	18	1.1	7545	8	AAI50282	AaI50282 Human nuc	c 207	17	1.0	239	4	AAH10044	AaH10044 Human cDN
c 135	18	1.1	10166	8	ABX76359	AbX76359 Lung canc	c 208	17	1.0	240	6	ABV88921	AbV88921 Human col
c 136	18	1.1	10166	8	ACD13432	AcD13432 Human DNA	c 209	17	1.0	241	6	ABQ49033	AbQ49033 Oligonuc
c 137	18	1.1	10166	11	ADN38843	AdN38843 Cancer/an	c 210	17	1.0	242	6	ABQ49032	AbQ49032 Oligonuc
c 138	18	1.1	10172	6	ABL65392	AbL65392 Lung canc	c 211	17	1.0	243	10	ADG76925	AdG76925 Hepatic
c 139	18	1.1	10172	12	ADQ18203	AdQ18203 Human sof	c 212	17	1.0	244	6	ABK35823	AbK35823 CDNA sequ
c 140	18	1.1	10175	5	AAST0589	AaST0589 DNA encod	c 213	17	1.0	245	6	ABL92616	AbL92616 Chlamydia
c 141	18	1.1	10284	8	ABX77543	AbX77543 Different	c 214	17	1.0	246	2	ADP43915	AdP43915 Chlamydia
c 142	18	1.1	10284	8	ABX63047	AbX63047 Human cDN	c 215	17	1.0	247	2	AAZ15236	AaZ15236 Human gen
c 143	18	1.1	10411	12	ADQ22757	AdQ22757 Human sof	c 216	17	1.0	248	6	ABQ38216	AbQ38216 Oligonuc
c 144	18	1.1	10853	12	ADQ22295	AdQ22295 Human sof	c 217	17	1.0	249	6	ABQ38217	AbQ38217 Oligonuc
c 145	18	1.1	10853	11	ADL27116	AdL27116 Human gen	c 218	17	1.0	250	2	AAI78167	AaI78167 Human den
c 146	18	1.1	14576	9	ADA03038	AdA03038 Human ROR	c 219	17	1.0	251	4	AAI95333	AaI95333 Human neu
c 147	18	1.1	14577	9	ADA66322	AdA66322 Human ROR	c 220	17	1.0	252	10	ADC78912	AdC78912 Human PRO
c 148	18	1.1	14577	10	ADB72776	AdB72776 Human ROR	c 221	17	1.0	253	11	ADCS5241	AdC55241 Human sig
c 149	18	1.1	110000	4	AAI99682_02	AaI99682_02	c 222	17	1.0	254	12	ADIS55241	AdI55241 Human sig
c 150	18	1.1	110000	6	AAI99683_02	AaI99683_02	c 223	17	1.0	255	6	ABL62626	AbL62626 Colom ade
c 151	18	1.1	110000	6	AAI99683_02	AaI99683_02	c 224	17	1.0	256	6	ABL68646	AbL68646 Kidney ca
c 152	18	1.1	110000	10	ACPF6367_10	AcPF6367_10	c 225	17	1.0	257	3	AAFI8330	AaFI8330 Lung canc
c 153	18	1.1	110000	10	ACPF6367_49	AcPF6367_49	c 226	17	1.0	258	6	ABT07742	AbT07742 Breast ca
c 154	18	1.1	110000	10	ACPF6367_0	AcPF6367_0	c 227	17	1.0	259	11	ADN39646	AdN39646 Cancer/an
c 155	18	1.1	110000	10	ACPF6367_4	AcPF6367_4	c 228	17	1.0	260	12	ADN04461	AdN04461 Antiporci
c 156	18	1.1	151826	3	AAI22291	AaI22291 BAC conta	c 229	17	1.0	261	10	ABX78332	AbX78332 Soybean s
c 157	18	1.1	151826	3	AAI22291	AaI22291 BAC conta	c 230	17	1.0	262	4	ABLI6017	AbLI6017 Drosophil
c 158	18	1.1	341511	6	AAH55200	AaH55200 Genomic D	c 231	17	1.0	263	8	ABA20661	AbA20661 Human ner
c 159	18	1.1	349980	5	AAH66829	AaH66829 C glutami	c 232	17	1.0	264	8	ACA19270	AcA19270 Prokaryot
c 160	18	1.1	349980	5	AAH66828	AaH66828 C glutami	c 233	17	1.0	265	6	ABN98968	AbN98968 Arabidops
c 161	17	1.0	25	9	ABV76847	AbV76847 Probe for	c 234	17	1.0	266	2	AAZ16375	AaZ16375 Human gen
c 162	17	1.0	25	9	ABV76847	AbV76847 Probe for	c 235	17	1.0	267	2	AAZ16375	AaZ16375 Human gen
c 163	17	1.0	25	9	ABV76847	AbV76847 Probe for	c 236	17	1.0	268	2	AAZ16375	AaZ16375 Human gen
c 164	17	1.0	47	10	ADCB7714	AdCB7714 Primer fo	c 237	17	1.0	269	11	ABD17107	AbD17107 Pseudom
c 165	17	1.0	60	6	ABN38582	AbN38582 Human spl	c 238	17	1.0	270	5	ADA32214	AdA32214 DNA encod
c 166	17	1.0	76	12	ACH84147	AcH84147 Human gen	c 239	17	1.0	271	5	AAH88024	AaH88024 DNA encod
c 167	17	1.0	149	3	AAI31853	AaI31853 Human sec	c 240	17	1.0	272	12	ADU44103	AdU44103 Plant cDN

241	17	1.0	983	4	AAI23433	Human bre	314	17	1.0	2634	4	ABL23066	Abi23066 Drosophila
C 242	17	1.0	1007	11	ADL80120	Rat GLAR2	C 315	17	1.0	2666	4	AAI61029	AAI61029 Human pol
C 243	17	1.0	1011	3	AACT6341	Human ORF	C 316	17	1.0	2674	5	ADL46031	ADL46031 Human ova
244	17	1.0	1026	10	ABX78323	Soybean s	317	17	1.0	2705	4	AAH17855	AAH17855 Human GDN
245	17	1.0	1044	3	AAc44684	Arabidops	318	17	1.0	2747	4	ABL13132	ABL13132 Drosophila
246	17	1.0	1083	3	AB214418	Arabidops	319	17	1.0	2781	11	ADM02100	ADM02100 Human GDN
247	17	1.0	1093	8	ADA68162	Arabidops	C 320	17	1.0	2799	4	AAI31406	AAI31406 Human GDN
C 248	17	1.0	1093	4	AAI663235	Arabidops	C 321	17	1.0	2799	6	ABQ66730	ABQ66730 Human pol
C 249	17	1.0	1095	1	ACH95859	Klebsiella	C 322	17	1.0	2799	10	ADCI0752	ADCI0752 Human GDN
C 250	17	1.0	1122	9	ADA31773	DNA encod	C 323	17	1.0	2822	11	ADM02578	ADM02578 Human GDN
C 251	17	1.0	1174	12	ADQ24977	Human sof	324	17	1.0	2834	10	ADF38007	ADF38007 Synchroni
252	17	1.0	1209	6	ABN67412	Streptoco	C 325	17	1.0	2931	1	AAH14627	AAH14627 Human GDN
253	17	1.0	1209	6	ABN69169	Streptoco	C 326	17	1.0	2975	4	ABQ69192	ABQ69192 Human GDN
254	17	1.0	1251	10	ADC93361	E. faeciu	327	17	1.0	2996	6	AAH16299	AAH16299 Human GDN
255	17	1.0	1314	3	AAI33762	Arabidops	C 328	17	1.0	2996	12	ADNO4821	ADNO4821 Antiporci
256	17	1.0	1341	12	ADM16727	PERL-P7-G	329	17	1.0	3044	4	AAI31284	AAI31284 Human GDN
C 257	17	1.0	1388	6	ABL65839	lung can	330	17	1.0	3044	6	ABQ66608	ABQ66608 Human pol
C 258	17	1.0	1388	6	ABL66504	lung can	331	17	1.0	3044	10	ADCI0630	ADCI0630 Human GDN
C 259	17	1.0	1389	10	ADA19248	Human ins	C 332	17	1.0	3081	4	AAH16266	AAH16266 Human GDN
C 260	17	1.0	1389	12	ADL7157	Human sol	C 333	17	1.0	3126	2	AAQ42425	AAQ42425 ADA3 DNA
C 261	17	1.0	1389	12	ADL71958	Human CEN	C 334	17	1.0	3132	11	ADM01994	ADM01994 Human GDN
C 262	17	1.0	1389	12	ADQ18940	Human sof	C 335	17	1.0	3145	9	ACH04114	ACH04114 Human GDN
C 263	17	1.0	1389	12	ADQ18940	Human sof	C 336	17	1.0	3246	5	ABV25849	ABV25849 Human pro
264	17	1.0	1434	3	AAI57987	1434 bp C	C 337	17	1.0	3247	5	ABV24853	ABV24853 Human pro
265	17	1.0	1438	3	AAI57944	1438 bp C	C 338	17	1.0	3406	4	ABL03126	ABL03126 Drosophila
266	17	1.0	1483	4	ABL13137	Drosophila	C 339	17	1.0	3469	4	ABL16016	ABL16016 Drosophila
C 267	17	1.0	1542	4	ABL29073	Drosophila	340	17	1.0	3536	4	ABL13136	ABL13136 Drosophila
C 268	17	1.0	1548	11	ABD17076	Pseudomon	341	17	1.0	3655	11	ADP09778	ADP09778 Complete
C 269	17	1.0	1551	10	ACC60634	Gene sequ	342	17	1.0	3715	10	ADA53498	ADA53498 Human cod
C 270	17	1.0	1551	10	ADK62575	Disease t	343	17	1.0	3805	4	ABL07900	ABL07900 Drosophila
C 271	17	1.0	1554	5	AAI577325	DNA encod	C 344	17	1.0	3846	4	ABA08642	ABA08642 Human ret
C 272	17	1.0	1587	3	AAI45864	Arabidops	345	17	1.0	3980	4	ABL24094	ABL24094 Drosophila
273	17	1.0	1591	3	AAI40192	Arabidops	C 346	17	1.0	4063	4	ABL18500	ABL18500 Drosophila
274	17	1.0	1626	9	ABD12546	Alloioioc	C 347	17	1.0	4071	6	ABO70833	ABO70833 Listeria
275	17	1.0	1626	9	ABD12546	Alloioioc	C 348	17	1.0	4140	8	ACD13197	ACD13197 CDNA enco
C 276	17	1.0	1647	10	ACF70647	Photothab	C 349	17	1.0	4149	6	ABK97892	ABK97892 DNA encod
C 277	17	1.0	1750	3	AAI286992	Retinobla	C 350	17	1.0	4226	4	AAI58593	AAI58593 Human pol
C 278	17	1.0	1803	12	ADQ23308	Human sof	C 351	17	1.0	4226	5	ADQ98810	ADQ98810 DNA encod
C 279	17	1.0	1806	10	ADCI3551	Human nov	C 352	17	1.0	4226	9	ADBA48570	ADBA48570 Novel hum
280	17	1.0	1871	6	ABL49882	Human euk	C 353	17	1.0	4238	4	ABL18076	ABL18076 Drosophila
281	17	1.0	1936	4	ABL18501	Drosophila	354	17	1.0	4264	4	AAI60379	AAI60379 Human pol
282	17	1.0	1936	10	ADK11422	Drosophila	C 355	17	1.0	4400	4	ABL29072	ABL29072 Drosophila
C 283	17	1.0	1980	4	ABL24095	Arabidops	C 356	17	1.0	4521	4	AAI59243	AAI59243 Human tra
C 284	17	1.0	2000	6	ABE16197	Arabidops	C 357	17	1.0	4674	5	ABA833068	ABA833068 Human GDN
C 285	17	1.0	2000	6	ABE16817	Arabidops	C 358	17	1.0	4933	10	ADP78188	ADP78188 Human ext
C 286	17	1.0	2000	6	ABE16817	Arabidops	C 359	17	1.0	5298	3	AACT6822	AACT6822 Human ORF
C 287	17	1.0	2000	8	ACC61539	Gene sequ	360	17	1.0	5411	10	ADB85523	ADB85523 Human GIG
C 288	17	1.0	2000	10	ADK64487	Disease t	361	17	1.0	5474	10	ADCI6738	ADCI6738 Human mod
C 289	17	1.0	2005	4	AAH15825	Human GDN	362	17	1.0	5474	2	AAQ90251	AAQ90251 Tubercous
C 290	17	1.0	2005	5	AAI193872	Human ato	363	17	1.0	5525	12	ADQ22998	ADQ22998 Human sof
C 291	17	1.0	2006	4	AAI31191	Human dia	364	17	1.0	5525	5	AAI76845	AAI76845 DNA encod
C 292	17	1.0	2018	4	AAI33608	Human car	365	17	1.0	5543	10	ADB85524	ADB85524 Human GIG
C 293	17	1.0	2018	10	ADE46762	Human car	366	17	1.0	5543	10	ADCI6739	ADCI6739 Human mod
C 294	17	1.0	2021	10	ADCI30797	Human nov	367	17	1.0	5543	12	ADQ18516	ADQ18516 Human sof
C 295	17	1.0	2063	4	ABL18077	Drosophila	368	17	1.0	5546	8	ADG42120	ADG42120 Human bra
C 296	17	1.0	2063	10	ADB62301	Human GDN	C 369	17	1.0	5659	8	ABX62964	ABX62964 Human act
C 297	17	1.0	2200	9	ADA09943	Plasmid K	370	17	1.0	5760	4	ABL17696	ABL17696 Drosophila
C 298	17	1.0	2200	11	ADL80088	Rat galan	C 371	17	1.0	5763	8	ABX62963	ABX62963 Human act
C 299	17	1.0	2200	12	ADG41992	Rat Galac	372	17	1.0	5778	4	AAK53086	AAK53086 Human pol
300	17	1.0	2235	8	AAI33680	Prokaryot	373	17	1.0	5804	4	AAK52102	AAK52102 Human pol
301	17	1.0	2237	4	ABL13285	Drosophila	C 374	17	1.0	6002	3	AAI2865968	AAI2865968 Retinobla
302	17	1.0	2260	8	ABE21288	Soybean n	375	17	1.0	6291	1	ABL06646	ABL06646 Drosophila
C 303	17	1.0	2260	8	ABE21288	Soybean n	C 376	17	1.0	6810	10	ADDO7807	ADDO7807 Novel cod
C 304	17	1.0	2271	4	AAH17984	Human GDN	C 377	17	1.0	6946	4	ABL26952	ABL26952 Drosophila
C 305	17	1.0	2273	3	AAI52462	HTM cion	C 378	17	1.0	7459	6	ABK31382	ABK31382 Signal tr
C 306	17	1.0	2300	2	AAI62735	Herbicide	379	17	1.0	7786	6	ABA92788	ABA92788 Buchnera
307	17	1.0	2346	12	ADQ18626	Human sof	C 380	17	1.0	8733	4	ABL29304	ABL29304 Drosophila
308	17	1.0	2346	12	ADQ18626	Human sof	C 381	17	1.0	11169	6	ABQ67095	ABQ67095 Human ang
309	17	1.0	2347	12	ADG32315	DNA encod	382	17	1.0	11622	6	ABL132675	ABL132675 Human imm
310	17	1.0	2385	3	AAI83331	PAR-1 pr	C 383	17	1.0	12595	4	AAI42100	AAI42100 Genomic s
C 311	17	1.0	2520	3	AAI83331	PAR-1 pr	C 384	17	1.0	13236	12	ADQ21058	ADQ21058 Human sof
C 312	17	1.0	2548	12	ADL27256	Human cod	C 385	17	1.0	13788	5	ABA19999	ABA19999 Human ner
313	17	1.0	2601	8	AAI36853	Prokaryot	386	17	1.0	13855	10	ADP79055	ADP79055 Human pro

C 387	17	1.0	15009	4	ABL13813	Abi13813 Drosophila	C 460	17	1.0	110000	12	ADH77486_01	Continuation (2 of
C 388	17	1.0	15330	5	ABAI5821	Abai5821 Human ner	C 461	17	1.0	110000	12	ADU75985_01	Continuation (2 of
C 389	17	1.0	15463	5	AAK86350	AAK86350 Human imm	C 462	17	1.0	110000	12	ADN97989_01	Continuation (2 of
C 390	17	1.0	18028	4	ABL13284	Abi13284 Drosophila	C 463	17	1.0	110000	12	ADOS0281_01	Continuation (2 of
C 391	17	1.0	19034	4	ABL13812	Abi13812 Drosophila	C 464	17	1.0	112600	12	AD018153	Adi13649 Oereocarth
C 392	17	1.0	19734	6	ABL33932	Abi33932 Human imm	C 465	17	1.0	127098	10	AD13649	Adi13649 Oereocarth
C 393	17	1.0	12798	10	ADD71026	Add71026 Human nch	C 466	17	1.0	134525	2	AAQ04525	AAQ04525 Total bas
C 394	17	1.0	22744	9	ADA02915	Ada02915 Mouse Fus	C 467	17	1.0	137507	2	AAV19941	AAV19941 KSHV long
C 395	17	1.0	22744	10	ADB72653	ADB72653 Mouse Fus	C 468	17	1.0	137508	12	ADN12162	Adn12162 Human her
C 396	17	1.0	22744	10	ADC85395	Adc85395 Mouse Fus	C 469	17	1.0	139032	6	ABQ79105	Abq79105 Human for
C 397	17	1.0	23744	12	ADM74510	Adm74510 Murine ca	C 470	17	1.0	139257	10	ADC89520	Adc89520 Human COR
C 398	17	1.0	24800	9	ADA02921	Ada02921 Mouse Ras	C 471	17	1.0	158091	12	ADL08119	Adl08119 Human gen
C 399	17	1.0	24800	10	ADB72659	ADB72659 Mouse Ras	C 472	17	1.0	162450	3	AAZ86967	Aaz86967 Retinobla
C 400	17	1.0	24800	10	ADC85401	Adc85401 Mouse Ras	C 473	17	1.0	174566	8	ABQ77400	Abq77400 Human ITG
C 401	17	1.0	24800	12	ADM74516	Adm74516 Murine ca	C 474	17	1.0	174566	12	ADL08118	Adl08118 Human gen
C 402	17	1.0	25231	4	AAI03112	AAI03112 Human rep	C 475	17	1.0	185035	6	ABT10147	Abt10147 Human bre
C 403	17	1.0	26201	6	ABK14446	Abk14446 Human HMP	C 476	17	1.0	185035	8	ACA64951	Ac64951 Human PEN
C 404	17	1.0	26201	6	ABK14039	Abk14039 Human 3-h	C 477	17	1.0	185035	12	ADO20284	Ado20284 Human sof
C 405	17	1.0	28001	12	ADI36729	Adi36729 Genomic D	C 478	17	1.0	197997	10	AAE54074	Aae54074 Human tra
C 406	17	1.0	28001	12	ADI36730	Adi36730 Genomic D	C 479	17	1.0	216215	10	ADF69167	Adf69167 Human MP5
C 407	17	1.0	28001	12	ADM93169	Adm93169 Human KOX	C 480	17	1.0	236303	4	AAI16137	Aai16137 Soybean 2
C 408	17	1.0	28001	12	ADM93170	Adm93170 Human KOX	C 481	17	1.0	335913	5	AAI61371	Aai61371 Soybean 2
C 409	17	1.0	29521	4	AAI32517	AAI32517 Human gen	C 482	17	1.0	335913	12	ADP20304	Adp20304 Human GPC
C 410	17	1.0	29543	4	AAK67239	AAK67239 Human imm	C 483	17	1.0	25	9	ACT64906	Act64906 Human mic
C 411	17	1.0	30393	4	AAK67239	AAK67239 Human imm	C 484	17	1.0	25	9	ACK11391	Ack11391 Human mic
C 412	17	1.0	32038	4	AAK90877	AAK90877 Human dig	C 485	17	1.0	25	9	ABZ43786	Abz43786 Human N-a
C 413	17	1.0	32038	4	AAK89980	AAK89980 Human dig	C 486	17	1.0	41	6	ABZ50823	Abz50823 Human N-a
C 414	17	1.0	32038	5	AAI30028	AAI30028 Human lun	C 487	17	1.0	60	6	ABN32576	Abn32576 Human gpl
C 415	17	1.0	32038	10	ADB33365	ADB33365 Human nov	C 488	17	1.0	65	6	ABN28763	Abn28763 Rat gplic
C 416	17	1.0	32844	12	ADJ12644	Adj12644 DNA fragm	C 489	17	1.0	88	12	ACH81606	Ach81606 Human gen
C 417	17	1.0	35100	2	AAV73802	AAV73802 KSHV LTR	C 490	17	1.0	88	12	ACH81606	Ach81606 Human gen
C 418	17	1.0	44147	6	ABK84481	Abk84481 Human CDN	C 491	17	1.0	112	4	AAI07391	Aai07391 Human rep
C 419	17	1.0	44147	9	ADD14691	Add14691 Human src	C 492	17	1.0	112	4	AAI07392	Aai07392 Human rep
C 420	17	1.0	50335	9	AAI58280	AAI58280 Human tum	C 493	17	1.0	112	4	ABA08195	AbA08195 Human ova
C 421	17	1.0	50385	9	AAK70336	AAK70336 Human imm	C 494	17	1.0	112	4	ABA08194	AbA08194 Human ova
C 422	17	1.0	52302	9	ADA02738	Ada02738 Human CCN	C 495	17	1.0	116	4	AAK17867	AAK17867 Human bra
C 423	17	1.0	52302	10	ADB72476	ADB72476 Human CCN	C 496	17	1.0	116	4	ABS43394	ABS43394 Human liv
C 424	17	1.0	52302	10	ADC85218	Adc85218 Human Ccn	C 497	17	1.0	129	4	ABA71834	AbA71834 Human foe
C 425	17	1.0	52302	12	ADM74533	Adm74533 Human car	C 498	17	1.0	129	4	AAI52178	Aai52178 Probe #20
C 426	17	1.0	54297	4	AAK70625	AAK70625 Human imm	C 499	17	1.0	129	4	AAK46279	AAK46279 Human bon
C 427	17	1.0	55001	12	ADG88848	Adg88848 Human Not	C 500	17	1.0	129	4	AAK20210	AAK20210 Human bra
C 428	17	1.0	55001	12	ADH74825	Adh74825 Human Not	C 501	17	1.0	129	4	ABS46001	ABS46001 Human liv
C 429	17	1.0	61355	10	ADC85996	Adc85996 Human GPC	C 502	17	1.0	129	6	ABS20593	ABS20593 Human gen
C 430	17	1.0	63359	6	AAI46665	AAI46665 Human tra	C 503	17	1.0	140	6	ABK39354	ABK39354 DNA encod
C 431	17	1.0	86000	12	ADP68568	Adp68568 Human PPA	C 504	17	1.0	140	8	ACA11683	ACA11683 Human lun
C 432	17	1.0	96597	9	ADA02597	Ada02597 Mouse Run	C 505	17	1.0	140	8	ACA02869	ACA02869 Lung canc
C 433	17	1.0	96597	10	ADB72335	ADB72335 Mouse Run	C 506	17	1.0	140	10	ADH46911	Adh46911 Human lun
C 434	17	1.0	96597	10	ADP58845	Adp58845 Mouse Run	C 507	17	1.0	144	4	ABA71779	AbA71779 Human foe
C 435	17	1.0	97658	8	ABO83210_3	Continuation (4 of	C 508	17	1.0	144	4	AAI52114	Aai52114 Probe #20
C 436	17	1.0	106344	10	ADJ79961	Adj79961 Full leng	C 509	17	1.0	144	4	AAK46208	AAK46208 Human bon
C 437	17	1.0	110000	2	AAV21209_10	Continuation (11 o	C 510	17	1.0	144	4	AAK20148	AAK20148 Human bra
C 438	17	1.0	110000	2	AAZ01425_06	Continuation (7 of	C 511	17	1.0	144	4	ABS45927	ABS45927 Human liv
C 439	17	1.0	110000	4	AAK95240_05	Continuation (2 of	C 512	17	1.0	144	6	ABS20519	ABS20519 Human gen
C 440	17	1.0	110000	4	AAI99682_00	AAI99682 Mycobacte	C 513	17	1.0	148	3	AAI27928	AAI27928 Human sec
C 441	17	1.0	110000	4	AAI99683_00	AAI99683 Mycobacte	C 514	17	1.0	156	6	ABS17802	ABS17802 Human gen
C 442	17	1.0	110000	4	AAK96733_01	Continuation (2 of	C 515	17	1.0	181	4	AAI25447	AAI25447 Human bre
C 443	17	1.0	110000	6	ABN71527_11	Continuation (12 o	C 516	17	1.0	194	4	AAI16604	Aai16604 Human bre
C 444	17	1.0	110000	6	ABN71527_20	Continuation (12 o	C 517	17	1.0	197	3	AAI60873	AAI60873 Human IRG
C 445	17	1.0	110000	6	ABO0010_01	Continuation (2 of	C 518	17	1.0	198	12	ACH92845	Ach92845 Human gen
C 446	17	1.0	110000	6	ABX08336_01	Continuation (2 of	C 519	17	1.0	199	2	AAI33750	AAI33750 Human DCR
C 447	17	1.0	110000	6	ABO69245_10	Continuation (11 o	C 520	17	1.0	200	2	AAV39190	AAV39190 Antifunga
C 448	17	1.0	110000	6	ABO67197_09	Continuation (10 o	C 521	17	1.0	204	12	ACH82417	Ach82417 Human gen
C 449	17	1.0	110000	6	ABO1503_01	Continuation (2 of	C 522	17	1.0	205	8	ABX47106	Abx47106 Bovine ES
C 450	17	1.0	110000	6	ABA03041_10	Continuation (11 o	C 523	17	1.0	206	2	AAQ11831	Aaq11831 17XD TNF
C 451	17	1.0	110000	6	ABA03041_16	Continuation (17 o	C 524	17	1.0	206	4	ABA66139	ABA66139 Human foe
C 452	17	1.0	110000	8	ABO83210_1	Continuation (2 of	C 525	17	1.0	206	4	AAI46323	AAI46323 Probe #15
C 453	17	1.0	110000	9	AAI53223_1	Continuation (2 of	C 526	17	1.0	206	4	ABS39875	ABS39875 Human liv
C 454	17	1.0	110000	9	ABDI2064_16	Continuation (17 o	C 527	17	1.0	206	6	ABSI14329	ABSI14329 Human gen
C 455	17	1.0	110000	10	ADF77343_09	Continuation (10 o	C 528	17	1.0	210	3	AAI54523	AAI54523 Human sec
C 456	17	1.0	110000	10	ACF67367_37	Continuation (38 o	C 529	17	1.0	214	2	AAT24795	Aat24795 Human gen
C 457	17	1.0	110000	11	ACF65388_10	Continuation (11 o	C 530	17	1.0	215	8	ABX45137	Abx45137 Bovine ES
C 458	17	1.0	110000	11	ADM27081_14	Continuation (15 o	C 531	17	1.0	220	12	ACH88040	Ach88040 Human sec
C 459	17	1.0	110000	11	ADM27081_15	Continuation (16 o	C 532	17	1.0	229	3	AAI25837	AAI25837 Human gen

533	16	1.0	234	10	ADH84057	Adh84057 Enterococ	606	16	1.0	352	5	AD168463	Ad168463 Human ova
534	16	1.0	237	5	ADL40139	Adl40139 Human ova	607	16	1.0	352	5	AD174829	Ad174829 Human ova
535	16	1.0	238	5	ABV20035	Abv20035 Human pro	608	16	1.0	353	3	AAA32070	Aaa32070 Plant mic
536	16	1.0	239	8	ABX54854	Abx54854 Bovine ES	609	16	1.0	353	4	AA180014	Aa180014 Human pol
537	16	1.0	242	2	AAO61034	Aao61034 Human bra	610	16	1.0	353	5	ADL40115	Adl40115 Human ova
538	16	1.0	246	2	AAAC16484	Aaac16484 Human sec	611	16	1.0	355	5	ABV02280	Abv02280 Human ova
539	16	1.0	249	8	ABV93957	Abv93957 Human col	612	16	1.0	355	5	AD168403	Ad168403 Human ova
540	16	1.0	250	2	AAV39187	Aav39187 Alfalfa p	613	16	1.0	355	5	AD174769	Ad174769 Human ova
541	16	1.0	250	5	AD174794	Ad174794 Human ova	614	16	1.0	355	6	ABK45916	Abk45916 CDNA enco
542	16	1.0	250	5	AD168428	Ad168428 Human ova	615	16	1.0	356	5	AD174821	Ad174821 Human ova
543	16	1.0	252	2	AA1740856	Aa1740856 Serine pr	616	16	1.0	356	5	AD168455	Ad168455 Human ova
544	16	1.0	252	2	AA1792853	Aa1792853 Flea sal1	617	16	1.0	357	4	AA136451	Aa136451 Human mus
545	16	1.0	252	2	AAV73401	Aav73401 Flea sal1	618	16	1.0	357	5	ADL40094	Adl40094 Human ova
546	16	1.0	252	4	AAAC0864	Aaac0864 Flea seer1	619	16	1.0	357	8	ABX59439	Abx59439 CDNA enco
547	16	1.0	255	5	AAH81956	Aah81956 Rat diffe	620	16	1.0	357	12	ADJ30189	Adj30189 Human mus
548	16	1.0	255	5	ADL40032	Adl40032 Human ova	621	16	1.0	360	5	AD174865	Ad174865 Human ova
549	16	1.0	256	4	AAK81668	Aak81668 Human imm	622	16	1.0	360	5	AD168501	Ad168501 Human ova
550	16	1.0	259	6	ABL71512	Ab171512 Corn tass	623	16	1.0	361	12	ADL11299	Adl11299 Cat flea
551	16	1.0	260	5	ABV58104	Abv58104 Human pro	624	16	1.0	361	12	ADP92942	Adp92942 Cotton ex
552	16	1.0	261	8	ABX55958	Abx55958 Bovine ES	625	16	1.0	362	5	ADL40060	Adl40060 Human ova
553	16	1.0	268	4	AA124580	Aa124580 Probe #14	626	16	1.0	363	5	AD174879	Ad174879 Human ova
554	16	1.0	268	4	ABA69751	Ab669751 Human foe	627	16	1.0	363	5	AD168515	Ad168515 Human ova
555	16	1.0	268	4	AA149836	Aa149836 Probe #18	628	16	1.0	364	9	ACH31759	Ach31759 Human bon
556	16	1.0	268	4	ABA36646	Ab36646 Probe #15	629	16	1.0	365	5	ADL40116	Adl40116 Human ova
557	16	1.0	268	4	AAK43821	Aak43821 Human bon	630	16	1.0	369	5	ADL42063	Adl42063 Human ova
558	16	1.0	268	4	AAK17944	Aak17944 Human bra	631	16	1.0	369	5	AD168560	Ad168560 Human ova
559	16	1.0	268	4	ABA43469	Ab43469 Human liv	632	16	1.0	369	5	AD174924	Ad174924 Human ova
560	16	1.0	268	6	ABS18048	Ab18048 Human gen	633	16	1.0	370	5	AD168562	Ad168562 Human ova
561	16	1.0	271	2	AAK32747	Aak32747 Human DCR	634	16	1.0	370	5	AD174926	Ad174926 Human ova
562	16	1.0	273	4	AA136127	Aa136127 Human mus	635	16	1.0	372	4	AA114631	Aa114631 Human bre
563	16	1.0	273	4	AA136128	Aa136128 Human mus	636	16	1.0	373	5	ADL40083	Adl40083 Human ova
564	16	1.0	273	8	ABX59116	Abx59116 CDNA enco	637	16	1.0	375	4	AA523971	Aa523971 Human ova
565	16	1.0	273	12	ABX59115	Abx59115 CDNA enco	638	16	1.0	375	4	AA525307	Aa525307 Human ova
566	16	1.0	273	12	ADJ29866	Adj29866 Human mus	639	16	1.0	378	5	AD168528	Ad168528 Human ova
567	16	1.0	273	12	ADJ29865	Adj29865 Human mus	640	16	1.0	378	5	AD174892	Ad174892 Human ova
568	16	1.0	277	2	AAK32749	Aak32749 Human DCR	641	16	1.0	381	4	AA550654	Aa550654 Human ova
569	16	1.0	277	5	ABV16923	Abv16923 Human pro	642	16	1.0	381	4	AA550738	Aa550738 Staphyloc
570	16	1.0	278	5	ADL40030	Adl40030 Human ova	643	16	1.0	381	8	ACAI17939	Acai17939 Prokaryot
571	16	1.0	282	12	ADL02521	Adl02521 DNA enco	644	16	1.0	381	8	ACAI18017	Acai18017 Prokaryot
572	16	1.0	283	2	AAK32752	Aak32752 Human DCR	645	16	1.0	386	5	AD168458	Ad168458 Human ova
573	16	1.0	287	3	AAK24946	Aak24946 Human sec	646	16	1.0	386	5	AD174824	Ad174824 Human ova
574	16	1.0	290	5	AD174793	Ad174793 Human ova	647	16	1.0	387	5	ABV13467	Abv13467 Human pro
575	16	1.0	290	5	AD168427	Ad168427 Human ova	648	16	1.0	387	5	AD168422	Ad168422 Human ova
576	16	1.0	295	8	ABX52749	Abx52749 Bovine ES	649	16	1.0	387	5	AD174921	Ad174921 Human ova
577	16	1.0	297	10	ADC90461	Adc90461 E. faeciu	650	16	1.0	387	5	AD174788	Ad174788 Human ova
578	16	1.0	304	5	ADL40031	Adl40031 Human ova	651	16	1.0	387	5	AD168557	Ad168557 Human ova
579	16	1.0	305	4	AAH73192	Aah73192 Human cer	652	16	1.0	387	6	ABQ91493	Abq91493 M. capsul
580	16	1.0	306	4	AAH70506	Aah70506 Human cer	653	16	1.0	390	5	AD174866	Ad174866 Human ova
581	16	1.0	312	5	AD168418	Ad168418 Human ova	654	16	1.0	390	5	AD168502	Ad168502 Human ova
582	16	1.0	312	5	AD174784	Ad174784 Human ova	655	16	1.0	390	8	ABX41411	Abx41411 Bovine ES
583	16	1.0	317	5	AD174834	Ad174834 Human ova	656	16	1.0	390	10	ADBS1050	Adbs1050 Primary x
584	16	1.0	317	5	AD168468	Ad168468 Human ova	657	16	1.0	393	3	AA565280	Aa565280 Pinus rad
585	16	1.0	322	5	AD174816	Ad174816 Human ova	658	16	1.0	393	12	ADK16186	Adk16186 Nanoarcha
586	16	1.0	322	5	AD168450	Ad168450 Human ova	659	16	1.0	394	5	AD168385	Ad168385 Human ova
587	16	1.0	324	5	AD168481	Ad168481 Human ova	660	16	1.0	394	5	AD174873	Ad174873 Human ova
588	16	1.0	324	5	AD174846	Ad174846 Human ova	661	16	1.0	394	5	AD174751	Ad174751 Human ova
589	16	1.0	325	5	ADL39996	Adl39996 Human ova	662	16	1.0	396	5	AA564828	Aa564828 Human ova
590	16	1.0	328	5	AD176827	Ad176827 Human ova	663	16	1.0	396	5	AA564828	Aa564828 Human ova
591	16	1.0	328	5	AD170502	Ad170502 Human ova	664	16	1.0	397	2	AAK07227	Aak07227 Human tum
592	16	1.0	329	5	ABA17354	Aba17354 Human ner	665	16	1.0	397	3	AAH30252	Aah30252 Human col
593	16	1.0	331	4	AAH69766	Aah69766 Human cer	666	16	1.0	397	3	ADL40006	Adl40006 Human ova
594	16	1.0	336	5	AA581434	Aa581434 DNA enco	667	16	1.0	398	4	AAH98237	Aah98237 Human EST
595	16	1.0	337	4	AAK70776	Aak70776 Human imm	668	16	1.0	398	9	ACH20610	Ach20610 Human adu
596	16	1.0	339	11	ADOS1600	Aaos1600 Human TAG	669	16	1.0	400	5	ADL40109	Adl40109 Human ova
597	16	1.0	340	4	AA538159	Aa538159 Novel hum	670	16	1.0	400	6	ABL66985	Ab166985 Thyroid c
598	16	1.0	341	5	ABA12330	Ab12330 Human ner	671	16	1.0	400	6	ABL68174	Ab168174 Kidney ca
599	16	1.0	344	5	AD174858	Ad174858 Human ova	672	16	1.0	401	5	AD168382	Ad168382 Human ova
600	16	1.0	344	5	AD168493	Ad168493 Human ova	673	16	1.0	401	5	AD174748	Ad174748 Human ova
601	16	1.0	347	5	AD174878	Ad174878 Human ova	674	16	1.0	402	5	ABV45856	Abv45856 Human pro
602	16	1.0	347	5	AD168514	Ad168514 Human ova	675	16	1.0	403	5	AD174809	Ad174809 Human ova
603	16	1.0	350	5	AD168558	Ad168558 Human ova	676	16	1.0	403	5	AD168443	Ad168443 Human ova
604	16	1.0	350	5	AD174922	Ad174922 Human ova	677	16	1.0	404	5	ADL40021	Adl40021 Human ova
605	16	1.0	351	4	AA189834	Aa189834 Human pol	678	16	1.0	404	5	AD168533	Ad168533 Human ova

679	16	1.0	404	5	AD174897	Human ova
680	16	1.0	405	5	AD168466	Human ova
681	16	1.0	405	5	AD174832	Human ova
c 682	16	1.0	406	5	ABV55043	Human pro
683	16	1.0	406	5	AD174765	Human ova
684	16	1.0	405	5	AD168399	Human ova
685	16	1.0	407	5	AD168491	Human ova
686	16	1.0	407	5	AD174872	Human ova
687	16	1.0	407	5	AD174856	Human ova
688	16	1.0	407	5	AD168508	Human ova
689	16	1.0	407	8	ABX35766	Bovine ES
690	16	1.0	407	10	ACD94192	Human
691	16	1.0	409	5	AD168555	Human ova
692	16	1.0	409	5	AD168400	Human ova
693	16	1.0	409	5	AD174919	Human ova
694	16	1.0	409	5	AD174766	Human ova
695	16	1.0	410	5	ABV32594	Human pro
696	16	1.0	410	5	ABV41519	Human pro
697	16	1.0	410	5	AD168473	Human ova
698	16	1.0	410	5	AD174838	Human ova
c 699	16	1.0	411	12	ACH71178	Human gen
c 700	16	1.0	412	9	ACH19279	Human
c 701	16	1.0	413	5	AA884687	DNA encod
c 702	16	1.0	413	5	AD174826	Human ova
703	16	1.0	413	5	AD168460	Human ova
c 704	16	1.0	414	5	ABV43439	Human pro
c 705	16	1.0	414	5	ABV34583	Human pro
706	16	1.0	416	5	AD168480	Human ova
707	16	1.0	416	5	AD168530	Human ova
708	16	1.0	416	5	AD174894	Human ova
709	16	1.0	416	5	AD174845	Human ova
c 710	16	1.0	417	4	AA137113	Human mus
c 711	16	1.0	417	8	ABX60101	CDNA
c 712	16	1.0	417	12	ADJ30851	Human mus
713	16	1.0	418	5	AD140161	Human ova
714	16	1.0	418	5	AD174907	Human ova
715	16	1.0	418	5	AD174901	Human ova
716	16	1.0	418	5	AD168543	Human ova
717	16	1.0	418	5	AD168537	Human ova
718	16	1.0	420	5	AD168409	Human ova
719	16	1.0	420	5	AD138810	Human ova
720	16	1.0	420	5	AD138811	Human ova
721	16	1.0	420	5	AD168511	Human ova
722	16	1.0	420	5	AD174775	Human ova
723	16	1.0	420	5	AD174875	Human ova
724	16	1.0	420	6	AB869513	Novel mur
725	16	1.0	421	5	AD168496	Human ova
726	16	1.0	421	5	AD140063	Human ova
727	16	1.0	421	5	AD168471	Human ova
728	16	1.0	421	9	ACH29641	Human tes
729	16	1.0	423	5	AD140163	Human ova
730	16	1.0	424	4	AA849850	Staphyloc
c 731	16	1.0	424	4	AB117993	Drosophil
732	16	1.0	424	8	ACA17118	Prokaryot
733	16	1.0	425	5	AD174852	Human ova
734	16	1.0	425	5	AD168487	Human ova
735	16	1.0	425	10	ADF80283	Leukemia
736	16	1.0	427	5	AD140110	Human ova
737	16	1.0	427	5	AD140095	Human ova
738	16	1.0	427	5	AD140093	Human ova
739	16	1.0	428	5	AD140066	Human ova
740	16	1.0	430	5	ABV46718	Human pro
741	16	1.0	430	5	AD168526	Human ova
742	16	1.0	430	5	AD168519	Human ova
743	16	1.0	430	5	AD174883	Human ova
744	16	1.0	430	5	AD174890	Human ova
745	16	1.0	432	4	AA113682	Human bre
746	16	1.0	433	4	AD174803	Human ova
747	16	1.0	433	5	AD168437	Human ova
748	16	1.0	433	5	AD174840	Human ova
749	16	1.0	434	5	AD168475	Human ova
750	16	1.0	434	5	AD140071	Human ova
c 751	16	1.0	436	8	ABX46922	Bovine ES
752	16	1.0	437	5	AD168479	Human ova
753	16	1.0	437	5	AD174844	Human ova
754	16	1.0	437	5	AD174849	Human ova
755	16	1.0	437	5	AD168484	Human ova
756	16	1.0	437	5	AD140134	Human ova
757	16	1.0	439	5	ABV11449	Human pro
758	16	1.0	440	9	ACH19597	Human
c 759	16	1.0	441	5	AA834277	Human
760	16	1.0	441	5	AD168516	Human ova
761	16	1.0	441	5	AD174880	Human ova
c 762	16	1.0	443	4	AA136260	Human mus
763	16	1.0	443	5	AD174817	Human ova
764	16	1.0	443	5	AD168451	Human ova
c 765	16	1.0	443	8	ABX59248	CDNA
c 766	16	1.0	443	12	ADJ29998	Human mus
767	16	1.0	446	5	AD140138	Human ova
768	16	1.0	447	5	AD140112	Human ova
769	16	1.0	447	9	ACH24778	Human adu
770	16	1.0	448	5	AD140058	Human ova
771	16	1.0	449	5	AD140053	Human ova
772	16	1.0	449	9	ACH27330	Human adu
773	16	1.0	451	5	AD168531	Human ova
774	16	1.0	451	5	AD174895	Human ova
775	16	1.0	452	4	ABAS9262	Human foe
776	16	1.0	452	4	AA139053	Probe #77
777	16	1.0	452	4	AAK33259	Human bon
778	16	1.0	452	4	AAK07474	Human bra
779	16	1.0	452	4	AB833009	Human liv
780	16	1.0	452	6	AB808091	Human gen
781	16	1.0	452	12	ADP94175	Colton ex
782	16	1.0	453	5	AD140131	Human ova
783	16	1.0	454	5	AD140117	Human ova
784	16	1.0	454	5	AD174889	Human ova
785	16	1.0	454	5	AD168525	Human ova
786	16	1.0	454	5	AD140102	Human ova
787	16	1.0	455	5	AD174749	Human ova
788	16	1.0	455	5	AD168383	Human ova
c 789	16	1.0	456	3	AAK09660	Human bec
790	16	1.0	457	5	AD140120	Human ova
791	16	1.0	458	4	ABAS3551	Human foe
792	16	1.0	458	4	AA131177	Probe #18
793	16	1.0	458	4	AAK05149	Human bra
794	16	1.0	458	4	AB826852	Human liv
795	16	1.0	458	4	AB830412	Human liv
796	16	1.0	458	5	AD174813	Human ova
797	16	1.0	458	5	AD140103	Human ova
798	16	1.0	458	5	AD168447	Human ova
799	16	1.0	458	6	AB801804	Human gen
800	16	1.0	459	2	AAK84621	Human TNF
801	16	1.0	459	3	AAK63757	Human TNF
802	16	1.0	459	12	AD115577	Human
803	16	1.0	459	12	AD021224	NOD2/CARD
c 804	16	1.0	460	9	ACH29129	Human adu
805	16	1.0	460	12	AD115575	Human
806	16	1.0	460	12	AD115584	Human NOD
807	16	1.0	460	12	AD115582	Human NOD
808	16	1.0	460	12	AD021229	NOD2/CARD
809	16	1.0	460	12	AD021231	NOD2/CARD
810	16	1.0	461	12	AD021222	NOD2/CARD
811	16	1.0	461	5	AD140061	Human ova
812	16	1.0	462	9	ACH34516	Human end
813	16	1.0	462	12	AD115576	Human NOD
814	16	1.0	462	12	AD115585	Human NOD
815	16	1.0	462	12	AD021223	NOD2/CARD
816	16	1.0	462	12	AD021232	NOD2/CARD
817	16	1.0	463	5	AD140016	Human ova
818	16	1.0	463	5	AD168421	Human ova
819	16	1.0	463	5	AD174787	Human ova
820	16	1.0	463	5	AD140025	Human ova
821	16	1.0	463	12	AD115586	Human NOD
822	16	1.0	463	12	AD021233	NOD2/CARD
823	16	1.0	464	5	AD174779	Human ova
824	16	1.0	464	5	AD168413	Human ova

825	16	1.0	464	9	ACH28090	898	16	1.0	490	5	ADL40077	Adl40077 Human ova
826	16	1.0	465	5	AD168436	899	16	1.0	491	2	AAx32745	AAx32745 Human DCR
827	16	1.0	465	5	AD174802	900	16	1.0	491	5	AD168551	Adl168551 Human ova
C 828	16	1.0	465	10	ADK55562	901	16	1.0	491	5	AD174915	Adl174915 Human ova
829	16	1.0	466	5	ADL41915	902	16	1.0	492	5	ADL40129	Adl40129 Human ova
830	16	1.0	466	12	ADL15580	903	16	1.0	493	5	ADL40127	Adl40127 Human ova
831	16	1.0	466	12	ADL15581	904	16	1.0	495	3	AACT5463	AACT5463 Human ORF
832	16	1.0	466	12	ADL15582	905	16	1.0	495	3	AACT5446	AACT5446 Arabidops
833	16	1.0	466	12	ADL15583	906	16	1.0	495	3	AACT5446	AACT5446 Arabidops
834	16	1.0	467	5	ADL40106	C 907	16	1.0	496	4	ABAS9322	ABAS9322 Human foe
835	16	1.0	467	12	ADL15578	C 908	16	1.0	496	4	AA139123	AA139123 Probe #78
836	16	1.0	467	12	ADL15579	C 909	16	1.0	496	4	AAK33336	AAK33336 Human bon
837	16	1.0	467	12	ADL15579	C 910	16	1.0	496	4	AAK07540	AAK07540 Human bra
838	16	1.0	467	12	ADL15579	C 911	16	1.0	496	4	ABAS33089	ABAS33089 Human liv
839	16	1.0	467	12	ADL15579	C 912	16	1.0	496	6	ABAS08171	ABAS08171 Human gen
840	16	1.0	467	12	ADL15579	C 913	16	1.0	496	9	ACH39708	ACH39708 Human foe
C 841	16	1.0	469	5	ABA08415	914	16	1.0	496	9	ACH39708	ACH39708 Human foe
842	16	1.0	469	5	AD168440	915	16	1.0	497	5	AD168541	AD168541 Human end
843	16	1.0	469	5	AD174806	916	16	1.0	497	5	AD174905	AD174905 Human ova
844	16	1.0	470	4	AA116133	917	16	1.0	497	12	ADL15574	ADL15574 Human ova
845	16	1.0	470	4	ABA58731	918	16	1.0	497	12	ADL15574	ADL15574 Human ova
846	16	1.0	470	4	AA138409	C 919	16	1.0	499	4	AAK92835	AAK92835 Human CDN
847	16	1.0	470	4	ABA27688	C 920	16	1.0	499	12	ADL29262	ADL29262 3' end of
848	16	1.0	470	4	AAK32589	C 921	16	1.0	500	5	ADL40132	ADL40132 Human ova
849	16	1.0	470	4	AAK06867	C 922	16	1.0	500	12	ACH68717	ACH68717 Human gen
850	16	1.0	470	4	ABAS32300	C 923	16	1.0	501	5	ABA14279	ABA14279 Human ner
851	16	1.0	470	6	ABAS07378	924	16	1.0	501	10	ABX07706	ABX07706 S. pneumo
852	16	1.0	471	5	AD174815	C 925	16	1.0	502	5	AAH82536	AAH82536 Human ova
853	16	1.0	471	5	AD168449	926	16	1.0	502	5	AD174920	AD174920 Human ova
854	16	1.0	471	5	ACH24722	927	16	1.0	502	5	AD168556	AD168556 Human ova
855	16	1.0	472	5	ADL40081	C 928	16	1.0	502	5	ADL40082	ADL40082 Human ova
856	16	1.0	472	5	ADL40974	C 929	16	1.0	503	3	AAAC99924	AAAC99924 Human sec
857	16	1.0	475	5	AD168472	C 930	16	1.0	504	6	ABO60717	ABO60717 Human col
858	16	1.0	475	5	ADL40054	931	16	1.0	504	4	AA111095	AA111095 Human bre
859	16	1.0	475	5	AD174837	932	16	1.0	504	5	AD174811	AD174811 Human ova
860	16	1.0	476	5	ADL39985	933	16	1.0	504	5	AD168381	AD168381 Human ova
861	16	1.0	477	5	ACH15881	934	16	1.0	504	5	AD174747	AD174747 Human ova
862	16	1.0	478	5	AD174912	935	16	1.0	504	5	ADL40076	ADL40076 Human ova
863	16	1.0	478	5	AD168548	936	16	1.0	504	5	AD168445	AD168445 Human ova
864	16	1.0	479	5	ADL40075	937	16	1.0	505	5	AD174847	AD174847 Human ova
865	16	1.0	480	2	AAQ62691	938	16	1.0	505	5	AD168482	AD168482 Human ova
866	16	1.0	480	3	AAQ62691	939	16	1.0	505	5	ADL40043	ADL40043 Human ova
C 867	16	1.0	480	5	AAK33403	940	16	1.0	507	2	AAV39195	AAV39195 Antifunga
868	16	1.0	480	5	ADL40003	941	16	1.0	507	5	AD174848	AD174848 Human ova
869	16	1.0	480	6	ABN72644	942	16	1.0	507	5	AD168412	AD168412 Human ova
870	16	1.0	480	9	ACH13921	943	16	1.0	507	5	AD168483	AD168483 Human ova
871	16	1.0	480	9	ACH26388	944	16	1.0	507	5	AD174778	AD174778 Human ova
872	16	1.0	480	9	ADAO8809	945	16	1.0	508	5	ADL40050	ADL40050 Human ova
873	16	1.0	480	10	ADPO8556	C 946	16	1.0	508	12	ACH67903	ACH67903 Human gen
874	16	1.0	480	10	ADG46304	947	16	1.0	509	5	ADL40086	ADL40086 Human ova
875	16	1.0	480	12	AD130096	948	16	1.0	509	5	ADL40088	ADL40088 Human ova
C 876	16	1.0	482	9	ACH34432	949	16	1.0	510	5	AD168545	AD168545 Human ova
C 877	16	1.0	482	10	ADDD32923	950	16	1.0	510	5	ADL40070	ADL40070 Human ova
C 878	16	1.0	483	5	AD174869	951	16	1.0	510	5	AD174909	AD174909 Human ova
879	16	1.0	483	5	AD174869	952	16	1.0	511	5	ADL40073	ADL40073 Human ova
880	16	1.0	483	5	ADL40002	953	16	1.0	513	5	ADL40089	ADL40089 Human ova
881	16	1.0	483	5	AD168505	954	16	1.0	513	5	ADL40159	ADL40159 Human ova
C 882	16	1.0	484	6	ABAS05302	955	16	1.0	513	5	AD168405	AD168405 Human ova
883	16	1.0	485	2	AAQ26994	956	16	1.0	513	5	AD174771	AD174771 Human ova
884	16	1.0	485	2	AAV05567	957	16	1.0	514	3	AAAC36860	AAAC36860 Arabidops
885	16	1.0	485	2	ACH34755	958	16	1.0	516	5	ADL40074	ADL40074 Human ova
C 886	16	1.0	486	4	AA113761	959	16	1.0	517	5	ADL40040	ADL40040 Human ova
C 887	16	1.0	486	4	AAK93804	960	16	1.0	517	5	ADL40052	ADL40052 Human ova
C 888	16	1.0	486	4	AAK91781	961	16	1.0	519	5	AD168444	AD168444 Human ova
C 889	16	1.0	486	5	ADL40085	962	16	1.0	519	5	AD174810	AD174810 Human ova
C 890	16	1.0	486	12	ADL28208	963	16	1.0	521	5	AD168439	AD168439 Human ova
C 891	16	1.0	486	12	ADL30231	964	16	1.0	521	5	ADL40084	ADL40084 Human ova
C 892	16	1.0	487	9	ADL40046	965	16	1.0	521	5	AD174805	AD174805 Human ova
C 893	16	1.0	487	9	ACH33337	C 966	16	1.0	522	12	ACH79145	ACH79145 Human gen
894	16	1.0	488	6	ABV97729	967	16	1.0	523	5	ADL40012	ADL40012 Human ova
895	16	1.0	488	6	ADL40156	968	16	1.0	524	5	AD174773	AD174773 Human ova
896	16	1.0	490	2	AAV39186	969	16	1.0	524	5	AD174851	AD174851 Human ova
897	16	1.0	490	5	ADL40039	970	16	1.0	524	5	AD168407	AD168407 Human ova

971	16	1.0	524	5	AD174839	Adi74839 Human ova
972	16	1.0	524	5	AD168486	Adi68486 Human ova
973	16	1.0	524	5	AD168474	Adi68474 Human ova
974	16	1.0	525	5	AD140069	Adi40069 Human ova
975	16	1.0	525	5	AD174764	Adi74764 Human ova
976	16	1.0	525	5	AD168398	Adi68398 Human ova
977	16	1.0	527	5	AD139886	Adi39886 Human ova
978	16	1.0	527	6	AB060704	Ab060704 Human col
979	16	1.0	528	6	ABV88075	Abv88075 Human col
980	16	1.0	529	6	AD141887	Adi41887 Human ova
981	16	1.0	529	6	ABQ59849	Abq59849 Human col
982	16	1.0	529	6	ABL83482	Abi83482 Human ova
983	16	1.0	529	6	AB137264	Abi37264 Human col
984	16	1.0	530	2	AAQ26895	AaQ26895 HCV gene
985	16	1.0	530	2	AAV05568	AaV05568 DNA as80C
986	16	1.0	531	6	AAa69695	AaA69695 Human ova
987	16	1.0	531	6	ABN72589	AbN72589 Ovarian c
988	16	1.0	531	6	ABK79052	AbK79052 Bacillus
989	16	1.0	531	9	ADA08754	Ada08754 Human ova
990	16	1.0	531	10	ADF08501	AdF08501 CDNA enco
991	16	1.0	531	10	ADG46249	AdG46249 Human ova
992	16	1.0	533	5	AD174836	Adi74836 Human ova
993	16	1.0	533	5	AD168470	Adi68470 Human ova
994	16	1.0	536	5	AD139888	Adi39888 Human ova
995	16	1.0	537	4	AAK87319	AaK87319 Human imm
996	16	1.0	538	5	AD174857	Adi74857 Human ova
997	16	1.0	538	5	AD168492	Adi68492 Human ova
998	16	1.0	542	3	AAc94996	AaC94996 Cat flea
999	16	1.0	546	4	ABa59802	AbA59802 Human foe
1000	16	1.0	546	4	AAK33949	AaK33949 Human bon

ALIGNMENTS

RESULT 1					
AAS01082					
ID	AAS01082 standard; DNA; 1641 BP.				
XX	AAS01082;				
AC	31-MAY-2001 (first entry)				
DT	Arabidopsis thaliana sterol acyltransferase LCAT2 DNA.				
XX	Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;				
KW	acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;				
KW	nutritional supplement; dairy product; food product; salad dressing; de.				
XX	Arabidopsis thaliana.				
OS	Key				
XX	CDS				
FT	Location/Qualifiers				
FT	1..1641				
FT	/*tag= a				
FT	/product= "LCAT2"				
XX	WO200116308-A2.				
PN	08-MAR-2001.				
XX	30-AUG-2000; 2000WO-US023863.				
XX	30-AUG-1999; 99US-0152493P.				
PR	(MONS) MONSANTO CO.				
XX	Laesner M, Van Benneham A;				
PI	WPI; 2001-169010/17.				
XX	P-PSDB; AAU00459.				
DR	New isolated nucleic acid encoding plant lecithin:cholesterol				
XX	acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase				
PT					

PT	-like polypeptides, for modifying the sterol content and oil production of plants.				
XX	Claim 5; Page 77; 127pp; English.				
PS	The present sequence encodes for Arabidopsis thaliana				
XX	lecithin:cholesterol acyltransferase-like 2 (LCAT2). Several novel				
CC	polynucleotides encoding the plant sterol acyltransferases LCAT				
CC	(AAS001081-AAS01104, AAS01341) and ACAT (acyl CoA:cholesterol				
CC	acyltransferase-like; AAS01311-AAS01319) are described. A yeast LCAT				
CC	related open reading frame, LROI gene sequence (AAS01342), and a rat ACAT				
CC	(AAS01105) cDNA sequence are also described. The polynucleotides encoding				
CC	LCAT or ACAT are used to produce LCAT or ACAT polypeptides. They can also				
CC	be used in a recombinant construct to transform a host cell (preferably				
CC	of a plant) or a plant. The recombinant construct is used to increase or				
CC	decrease the sterol content of the host cell or plant. It can be used to				
CC	alter oil production of the cell or plant, preferably by increasing it.				
CC	The oil of the plant or the plant itself is used as a food product, or as				
CC	nutritional or dietary supplements, or in pharmaceutical compositions for				
CC	lowering cholesterol. The oil can be used in foods e.g. margarine,				
CC	butter, cooking oil, and dressings e.g. salad dressings, mayonnaise,				
CC	cheese, processed meat, pasta, sauces, cereals, desserts, dips, chips,				
CC	baked goods, pastries, cookies, snack bars, confections, chocolates, and				
CC	beverages. The alteration in sterol content and/or composition can also				
CC	provide a plant with tolerance to stress and insect damage				
XX	Sequence 1641 BP; 438 A; 355 C; 378 G; 470 T; 0 U; 0 Other;				
SQ					
Query Match	100.0%;	Score 1641;	DB 5;	Length 1641;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 1641;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 ATGGAGCGAATTCGAATACGTAACGCGCTTCCTCAACCGTCATCGCCGTTTTCTTG 60				
DB	1 ATGGAGCGAATTCGAATACGTAACGCGCTTCCTCAACCGTCATCGCCGTTTTCTTG 60				
QY	61 ATTGGCGTGCGCAACCTCGCGGTGAGATGAGCCGAGTTCCACGGGACTACCTCGAG 120				
DB	61 ATTGGCGTGCGCAACCTCGCGGTGAGATGAGCCGAGTTCCACGGGACTACCTCGAG 120				
QY	121 CTATCGGGTAAATCATCTCCGGGATTTGCGTCGACGACGTACGAGCGTGCATCTT 180				
DB	121 CTATCGGGTAAATCATCTCCGGGATTTGCGTCGACGACGTACGAGCGTGCATCTT 180				
QY	181 GACTGTCCATACACTCCGTTGAGCTTCAATCCGCTCGACTGTATGCTAGACCACT 240				
DB	181 GACTGTCCATACACTCCGTTGAGCTTCAATCCGCTCGACTGTATGCTAGACCACT 240				
QY	241 AAGCTCTCTTCTGCTGCAACTGCTGTTAAGTATGCTAGATCCCTTAATGAA 300				
DB	241 AAGCTCTCTTCTGCTGCAACTGCTGTTAAGTATGCTAGATCCCTTAATGAA 300				
QY	301 ACAGACCATCCCGAGTATGATGACGAGCTGACAGTGTCTTTCAGCCATCAGAAATTG 360				
DB	301 ACAGACCATCCCGAGTATGATGACGAGCTGACAGTGTCTTTCAGCCATCAGAAATTG 360				
QY	361 GATCCAGTTACATTAACAGTCTCTTTCTAATCTGTCTGAAAGAGTGCTTAAGTGCT 420				
DB	361 GATCCAGTTACATTAACAGTCTCTTTCTAATCTGTCTGAAAGAGTGCTTAAGTGCT 420				
QY	421 GTTAGTTTGGTATAGAAAGCAAAATGCAATGTCTGCTGTTCATAGATTGAGATTGCA 480				
DB	421 GTTAGTTTGGTATAGAAAGCAAAATGCAATGTCTGCTGTTCATAGATTGAGATTGCA 480				
QY	481 CCAACCAAAATTGGAAGAGCGTGAACCTTACTTTACAAAGTCAAGTTGACCTTTGAACT 540				
DB	481 CCAACCAAAATTGGAAGAGCGTGAACCTTACTTTACAAAGTCAAGTTGACCTTTGAACT 540				
QY	541 GCTTTAAAACTCGGTGCGCGCCCTTCTATAGATTGCGCATTCATGGGTAATATGTC 600				
DB	541 GCTTTAAAACTCGGTGCGCGCCCTTCTATAGATTGCGCATTCATGGGTAATATGTC 600				
QY	601 TTCAGATACCTTTCGGAATGCTGAGGCTAGAAATTCGACCAAAACATTAATTGAAATG 660				

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Db      |||
601 TTGAGATACCTTTCGAAATGAGCTGAGGCTAGAGAAATGACCAAAACATTAATTGAAGGG 660
Qy      |||
661 CTGATACAGCATATCCATGCTTATTTGCGTGTGAGCTCTCTTTGGTCTGTGAG 720
Db      |||
661 CTGATACAGCATATCCATGCTTATTTGCGTGTGAGCTCTCTTTGGTCTGTGAG 720
Qy      |||
721 GCATCAAAATCTACTCTCTGTGTAAAGTTGGCCCTCTGTTCTGAGGAACTGCT 780
Db      |||
721 GCATCAAAATCTACTCTCTGTGTAAAGTTGGCCCTCTGTTCTGAGGAACTGCT 780
Qy      |||
781 CGGTGTGTTCCAATCTTTTGGCGTGTGATGTGGCTTATGCAATTTCAAAGAAATTC 840
Db      |||
781 CGGTGTGTTCCAATCTTTTGGCGTGTGATGTGGCTTATGCAATTTCAAAGAAATTC 840
Qy      |||
841 AAGGTGATTAACATCTGAGACCATTTTCTGGGGGTGTGCAAAAGAAATGAGGCC 900
Db      |||
841 AAGGTGATTAACATCTGAGACCATTTTCTGGGGGTGTGCAAAAGAAATGAGGCC 900
Qy      |||
901 GTATACCACTGTGATGAAAGAAATATCAATCAAAATATTTCTGGCTGGCCGCAAAATAT 960
Db      |||
901 GTATACCACTGTGATGAAAGAAATATCAATCAAAATATTTCTGGCTGGCCGCAAAATAT 960
Qy      |||
961 ATTAACATTAATTCCTTCCATGAGCGTTACAGAAACAGCTTAGTCAACATGACGAC 1020
Db      |||
961 ATTAACATTAATTCCTTCCATGAGCGTTACAGAAACAGCTTAGTCAACATGACGAC 1020
Qy      |||
1021 ATGGAATGTGGCCCTCCCAACCTTTTGTCTTTCACAGCCCGTGAATAGAGATGGGACT 1080
Db      |||
1021 ATGGAATGTGGCCCTCCCAACCTTTTGTCTTTCACAGCCCGTGAATAGAGATGGGACT 1080
Qy      |||
1081 CTTTTCAAAGCATAGAAAGATATGATGACCCAGATAGCAAGATGTTTACACAGTTAAG 1140
Db      |||
1081 CTTTTCAAAGCATAGAAAGATATGATGACCCAGATAGCAAGATGTTTACACAGTTAAG 1140
Qy      |||
1141 AAGTGTATCATGATGACCTCTGTTTAAATCCTCTGACTCTTGGAGAGACCACTATA 1200
Db      |||
1141 AAGTGTATCATGATGACCTCTGTTTAAATCCTCTGACTCTTGGAGAGACCACTATA 1200
Qy      |||
1201 AAAAATGATTTTTCATATGAGTGCATCTTAAAGACAGAGTGGTATTAATCTTGGCC 1260
Db      |||
1201 AAAAATGATTTTTCATATGAGTGCATCTTAAAGACAGAGTGGTATTAATCTTGGCC 1260
Qy      |||
1261 CCAAGTGGCAAAACCTTATCTGATATGATGATCAACGATATCATTTAGAACTGAA 1320
Db      |||
1261 CCAAGTGGCAAAACCTTATCTGATATGATGATCAACGATATCATTTAGAACTGAA 1320
Qy      |||
1321 GGTTCCTCGTGTCAAGGTCTGAACTGTGTGATGAGGAAACGCTGACCTATACTGGG 1380
Db      |||
1321 GGTTCCTCGTGTCAAGGTCTGAACTGTGTGATGAGGAAACGCTGACCTATACTGGG 1380
Qy      |||
1381 GATAGACGGTAAACCTTATCATCTCTCTTGGTGCAGAAATTTGGCTGGACCTAAAGTT 1440
Db      |||
1381 GATAGACGGTAAACCTTATCATCTCTCTTGGTGCAGAAATTTGGCTGGACCTAAAGTT 1440
Qy      |||
1441 AACATAACAATGGCTCCCGACCCAGAACAGATGAGGAGCGATGATGGAATTAAT 1500
Db      |||
1441 AACATAACAATGGCTCCCGACCCAGAACAGATGAGGAGCGATGATGGAATTAAT 1500
Qy      |||
1501 GTTGATCATGAGCATGGGTGAGACATCATTAAGCAAAAGCAAAAGGCTTAAG 1560
Db      |||
1501 GTTGATCATGAGCATGGGTGAGACATCATTAAGCAAAAGCAAAAGGCTTAAG 1560
Qy      |||
1561 TACATAACCTTTTATGAAAGATCTGAGAGCAATTCGGGGAAAGAAACCGCAGTCTGGAG 1620
Db      |||
1561 TACATAACCTTTTATGAAAGATCTGAGAGCAATTCGGGGAAAGAAACCGCAGTCTGGAG 1620
Qy      |||
1621 CTTGATAAAGTGGTATTA 1641
Db      |||
1621 CTTGATAAAGTGGTATTA 1641

```

RESULT 2

```

ADP47823
ID ADP47823 standard; DNA; 1902 BP.
XX
AC ADP47823;
XX
DT 26-FEB-2004 (first entry)
XX
DE Arabidopsis thaliana acyltransferase nucleotide sequence SEQ ID NO:8.
XX
KW acyltransferase; enzyme; membrane-spanning region;
KW active membrane independent acyltransferase; fatty acid ester;
KW fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol;
KW phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;
KW acylated amino acid; structured lipid; fat-soluble molecule; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN W02003100044-A1.
XX
PD 04-DEC-2003.
XX
PE 28-MAY-2003; 2003WO-SB000870.
XX
PR 29-MAY-2002; 2002SE-00001581.
PR 29-MAY-2002; 2002US-0383889P.
PR 20-JAN-2003; 2003SE-00000142.
XX
PA (SCAN-) SCANDINAVIAN BIOTECHNOLOGY RES AB.
XX
PI Dahlqvist A, Ghosal A, Lindqvist Y, Banas A;
XX
DR WPI; 2004-053268/05.
XX
DR P-PSDB; ADP47824.
XX
PT New nucleotide sequence encoding an improved acyltransferase polypeptide,
PT useful for producing structured lipids or fat-soluble molecules, in
PT removing undesirable fat or in modifying lipids in animal or plant raw
PT material.
XX
PS Claim 5; SEQ ID NO 8; 91pp: English.
XX
CC The present invention describes a nucleotide sequence (I) derived from a
CC nucleotide sequence encoding an acyltransferase polypeptide comprising at
CC least one membrane-spanning region. (II) encodes an improved active
CC membrane independent acyltransferase polypeptide in which at least one
CC amino acid residue of the membrane-spanning region has been deleted
CC and/or substituted as compared to the original acyltransferase
CC polypeptide, where the encoded active membrane independent
CC acyltransferase polypeptide can produce fatty acid esters and/or fatty
CC acid thioesters such as triacylglycerols, diacylglycerols,
CC monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters,
CC acylated carbohydrates and acylated amino acids. Also described: (1) a
CC nucleotide sequence molecule (II) comprising at least one promoter region
CC which functions in a host, where the promoter region is operably linked
CC to at least one (I), which is operably linked to at least one non-
CC translated region which functions in a host; (2) a vector comprising (II)
CC; (3) a host cell comprising (II) or the vector; (4) producing an
CC improved active membrane independent acyltransferase polypeptide,
CC comprising providing the above host cell and a growth medium preparing a
CC host cell culture, culturing the host cell culture and harvesting the
CC host cell culture and recovering the improved active membrane independent
CC acyltransferase polypeptide; (5) a polypeptide obtained by the method in
CC (4), where the polypeptide at least is an improved active membrane
CC independent acyltransferase polypeptide; (6) an oligonucleotide
CC specifically hybridizing to (I) under stringent conditions; and (7) a kit
CC comprising the above polypeptide and a stabiliser. The nucleic acid
CC molecule (I) and the polypeptide are useful in producing structured
CC lipids or fat-soluble molecules, in removing undesirable fat or in
CC modifying lipids present in animal and plant raw material. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 1902 BP; 516 A; 405 C; 444 G; 537 T; 0 U; 0 Other;

```

Query Match 83.8%; Score 1375; DB 12; Length 1902;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGAGGGAATTCGAAATCAGTACGGCTTCCTTACCGTCAATGCGGCTTTTCTCTG 60
DB 1 ATGGAGGGAATTCGAAATCAGTACGGCTTCCTTACCGTCAATGCGGCTTTTCTCTG 60
QY 61 ATTTGCGGTGGCCGAACCTGCGGTGAGAGATGAGACGAGTTTCAACGCGACTACTCGAAG 120
DB 61 ATTTGCGGTGGCCGAACGCGGTGAGAGATGAGACGAGTTTCAACGCGACTACTCGAAG 120
QY 121 CTATGCGGTATATATATTCCTGGGATTTGCGTCAAGCAGCTACGAGCGTGGTCCATCTT 180
DB 121 CTATGCGGTATATATATTCCTGGGATTTGCGTCAAGCAGCTACGAGCGTGGTCCATCTT 180
QY 181 GACTGTCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTGAGACCACT 240
DB 181 GACTGTCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTGAGACCACT 240
QY 241 AAGCTTCTTTCGTCTGCTCACTGCTGTTTAAAGTATGCTAGATCTTATATCA 300
DB 241 AAGCTTCTTTCGTCTGCTCACTGCTGTTTAAAGTATGCTAGATCTTATATCA 300
QY 301 ACAGACCATCCCGAGTGAAGTCAAGCCTGACAGTGGTCTTTGACCATACAGAAATG 360
DB 301 ACAGACCATCCCGAGTGAAGTCAAGCCTGACAGTGGTCTTTGACCATACAGAAATG 360
QY 361 GATCCAGGTTACATAACAGGCTCTTCTACTGCTGGAAGAAGTGGCTTAAGTGGT 420
DB 361 GATCCAGGTTACATAACAGGCTCTTCTACTGCTGGAAGAAGTGGCTTAAGTGGT 420
QY 421 GTTGAGTTTGGTATGAGAACAAATGCAATGTCGCTGTTCCATACGATTGAGATGTC 480
DB 421 GTTGAGTTTGGTATGAGAACAAATGCAATGTCGCTGTTCCATACGATTGAGATGTC 480
QY 481 CCAACCAATTTGGAAGAGCTGACCTTTACTTTCACAGCTCAAGTGAAGCTTTGAAACT 540
DB 481 CCAACCAATTTGGAAGAGCTGACCTTTACTTTCACAGCTCAAGTGAAGCTTTGAAACT 540
QY 541 GCTTTAAACCTCCGAGGCGCCCTCTATAGATTATGGCCATTCAATGGGTAAATGATGTC 600
DB 541 GCTTTAAACCTCCGAGGCGCCCTCTATAGATTATGGCCATTCAATGGGTAAATGATGTC 600
QY 601 TTCAAGATATCTTCTGGAATGCGTGAAGCTAGAAATGCAACAAACATTAATTTGAAGTGG 660
DB 601 TTCAAGATATCTTCTGGAATGCGTGAAGCTAGAAATGCAACAAACATTAATTTGAAGTGG 660
QY 661 CTTGATCAGCATATCAGTCTTATTTGCTGTTGAGACTCTCTTCTTGGTTCTGTTAG 720
DB 661 CTTGATCAGCATATCAGTCTTATTTGCTGTTGAGACTCTCTTCTTGGTTCTGTTAG 720
QY 721 GCAATCAATCACTCTCTGCTGCTGTAAGTGGCTTCCGTTCTGAGGGAATGCT 780
DB 721 GCAATCAATCACTCTCTGCTGCTGTAAGTGGCTTCCGTTCTGAGGGAATGCT 780
QY 781 CCGTTGTTGTCGAATTTCTTTTGGCGTCAATGTTGCTTAAGCCATTTTCAAGAATGTC 840
DB 781 CCGTTGTTGTCGAATTTCTTTTGGCGTCAATGTTGCTTAAGCCATTTTCAAGAATGTC 840
QY 841 AAGGATGATTAACATCTCTGACGCAATTTTCTGGGGGTGCTGCAAAAGAAATAGCGC 900
DB 841 AAGGATGATTAACATCTCTGACGCAATTTTCTGGGGGTGCTGCAAAAGAAATAGCGC 900
QY 901 GTATACCACTGATGAAGAGAAATATCAATCAAAATTTCTGGCTGGCCGCAAAATTT 960
DB 901 GTATACCACTGATGAAGAGAAATATCAATCAAAATTTCTGGCTGGCCGCAAAATTT 960
QY 961 ATTTAATTTGAATTTCTTTCACAGCTTACAGAAACAGCTCTAGTCAACATGACGAC 1020
DB 961 ATTTAATTTGAATTTCTTTCACAGCTTACAGAAACAGCTCTAGTCAACATGACGAC 1020
QY 1021 ATGGAATGAGCTTCCACCTTTTGTCTTTCACAGCCCGTGAATGACAGATGGAGCT 1080

DB 1021 ATGGAATGAGCTTCCACCCCTTTTGTCTTTCACAGCCCGTGAATGACAGATGGAGCT 1080
QY 1081 CTTTTCAGCAATAGAAAGCTATGACCCAGATGCAAGAGATGTTTACACAGTTAAAG 1140
DB 1081 CTTTTCAGCAATAGAAAGCTATGACCCAGATGCAAGAGATGTTTACACAGTTAAAG 1140
QY 1141 AAGTTGATCATGATGACCCCTGTTTTTAACTCTGACTCTCTGGAGAGACCACTATA 1200
DB 1141 AAGTTGATCATGATGACCCCTGTTTTTAACTCTGACTCTCTGGAGAGACCACTATA 1200
QY 1201 AAAAATGATTTTGCATATATGAGTCTCATCTATAAGACAGAGTTGTTATTACTTGGC 1260
DB 1201 AAAAATGATTTTGCATATATGAGTCTCATCTATAAGACAGAGTTGTTATTACTTGGC 1260
QY 1261 CCAAGTGGCAAACTTTATCCGATATATGATCATCAAGATATCATTTACGAAACTGAA 1320
DB 1261 CCAAGTGGCAAACTTTATCCGATATATGATCATCAAGATATCATTTATGAAACTGAA 1320
QY 1321 GGTTCCTCGTGTCAAGTCTGGAACGTGTGTTGATGAGAAACGCTGACCTATACTGGG 1380
DB 1321 GGTTCCTCGTGTCAAGTCTGGAACGTGTGTTGATGAGAAACGCTGACCTATACTGGG 1380
QY 1381 GATGAGACGGTACCTTATCATTCATCTCTTGGTGAAGAAATGCTGAGACTTAAGTT 1440
DB 1381 GATGAGACGGTACCTTATCATTCATCTCTTGGTGAAGAAATGCTGAGACTTAAGTT 1440
QY 1441 AACATAACAAATGAGTCCCGACCGACAGAACAGATGGAAGCGATACATGTTGAACTAAAT 1500
DB 1441 AACATAACAAATGAGTCCCGACCGACAGAACAGATGGAAGCGATACATGTTGAACTAAAT 1500
QY 1501 GTTGATCATGAGCATGAGTGCATCATATGACTTAACATGACAAAGACCAAGGTTAAG 1560
DB 1501 GTTGATCATGAGCATGAGTGCATCATATGACTTAACATGACAAAGACCAAGGTTAAG 1560
QY 1561 TACATAACCTTTTATGAAAGCTCGAGAGCAATTCGAGGGAAGAGAACCGAGTCTGGAG 1620
DB 1561 TACATAACCTTTTATGAAAGCTCGAGAGCAATTCGAGGGAAGAGAACCGAGTCTGGAG 1620
QY 1621 CTTGATTAATA 1630
DB 1621 CTTGATTAATA 1630

RESULT 3
AAC6438
ID AAC6438 standard; DNA; 3896 BP.
XX
AC AAC6438;
DT 12-FEB-2001 (first entry)
XX
DE Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:11.
XX
KW PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
XX EST; expressed sequence tag; fatty acid; oil content; de.
XX Arabidopsis thaliana.
OS
PN WO20060095-A2.
XX
PD 12-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-EP002701.
XX
PR 01-APR-1999; 99EP-0010655.
PR 10-JUN-1999; 99EP-00111321.
PR 07-FEB-2000; 2000US-0180687P.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Dahlqvist A, Stahl U, Lenman M, Banas A, Romne H, Stymne S;


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PA (MONS ) MONSANTO CO.
XX
XX Laesner M, Van Eenennaam A;
XX
XX WPI; 2001-169010/17.
DR
XX New isolated nucleic acid encoding plant lecithin:cholesterol
XX acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase
XX -like polypeptides, for modifying the sterol content and oil production
XX of plants.
XX
XX Example 4; Page 36; 127pp; English.
XX
XX The present sequence for LCAT2 PCR primer #1 is used with PCR primer #2
XX (AAS01323) to amplify Arabidopsis thaliana lecithin:cholesterol
XX acyltransferase-like 2 (LCAT2). The PCR product is used to prepare an
XX expression construct. Several novel polynucleotides encoding the plant
XX sterol acyltransferases LCAT (AAS001081-AAS01104, AAS01341) and ACAT
XX (acyl CoA:cholesterol acyltransferase-like; AAS01311-AAS01319) are
XX described. A yeast LCAT related open reading frame, LRO1 gene sequence
XX (AAS01342), and a rat ACAT (AAS01105) cDNA sequence are also described.
XX The polynucleotides encoding LCAT or ACAT are used to produce LCAT or
XX ACAT polypeptides. They can also be used in a recombinant construct to
XX transform a host cell (preferably of a plant) or a plant. The recombinant
XX construct is used to increase or decrease the sterol content of the host
XX cell or plant. It can be used to alter oil production of the cell or
XX plant, preferably by increasing it. The oil of the plant or the plant
XX itself is used as a food product, or as nutritional or dietary
XX supplements, or in pharmaceutical compositions for lowering cholesterol.
XX The oil can be used in foods e.g. margarine, butter, cooking oil, and
XX dressings e.g. salad dressings, mayonnaise, cheese, processed meat,
XX pasta, sauces, cereals, desserts, dips, chips, baked goods, pastries,
XX cookies, snack bars, confections, chocolates, and beverages. The
XX alteration in sterol content and/or composition can also provide a plant
XX with tolerance to stress and insect damage
XX
XX Sequence 44 BP; 13 A; 11 C; 14 G; 6 T; 0 U; 0 Other;
SO
Query Match 1.6%; Score 27; DB 5; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGGAGGCAATTCGAATCACTACG 27
DB 18 ATGGAGGCAATTCGAATCACTACG 44

```

RESULT 6

AAS01323/C

ID AAS01323 standard; DNA; 40 BP.

AC AAS01323;

XX

DT 31-MAY-2001 (first entry)

DE Arabidopsis thaliana LCAT2 coding sequence PCR primer #2.

XX

KW Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;

KW acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;

KW nutritional supplement; dairy product; food product; salad dressing;

KW PCR primer; sb.

XX

XX Arabidopsis thaliana.

OS

PN WO200116308-A2.

XX

PD 08-MAR-2001.

XX

PF 30-AUG-2000; 2000WO-US023863.

XX

PR 30-AUG-1999; 99US-0152493P.

XX

PA (MONS) MONSANTO CO.

```

XX
XX Laesner M, Van Eenennaam A;
XX
XX WPI; 2001-169010/17.
DR
XX New isolated nucleic acid encoding plant lecithin:cholesterol
XX acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase
XX -like polypeptides, for modifying the sterol content and oil production
XX of plants.
XX
XX Example 4; Page 36; 127pp; English.
XX
XX The present sequence for LCAT2 PCR primer #2 is used with PCR primer #1
XX (AAS01322) to amplify Arabidopsis thaliana lecithin:cholesterol
XX acyltransferase-like 2 (LCAT2). The PCR product is used to prepare an
XX expression construct. Several novel polynucleotides encoding the plant
XX sterol acyltransferases LCAT (AAS001081-AAS01104, AAS01341) and ACAT
XX (acyl CoA:cholesterol acyltransferase-like; AAS01311-AAS01319) are
XX described. A yeast LCAT related open reading frame, LRO1 gene sequence
XX (AAS01342), and a rat ACAT (AAS01105) cDNA sequence are also described.
XX The polynucleotides encoding LCAT or ACAT are used to produce LCAT or
XX ACAT polypeptides. They can also be used in a recombinant construct to
XX transform a host cell (preferably of a plant) or a plant. The recombinant
XX construct is used to increase or decrease the sterol content of the host
XX cell or plant. It can be used to alter oil production of the cell or
XX plant, preferably by increasing it. The oil of the plant or the plant
XX itself is used as a food product, or as nutritional or dietary
XX supplements, or in pharmaceutical compositions for lowering cholesterol.
XX The oil can be used in foods e.g. margarine, butter, cooking oil, and
XX dressings e.g. salad dressings, mayonnaise, cheese, processed meat,
XX pasta, sauces, cereals, desserts, dips, chips, baked goods, pastries,
XX cookies, snack bars, confections, chocolates, and beverages. The
XX alteration in sterol content and/or composition can also provide a plant
XX with tolerance to stress and insect damage
XX
XX Sequence 40 BP; 9 A; 14 C; 6 G; 11 T; 0 U; 0 Other;
SO
Query Match 1.6%; Score 26; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1616 GGGAGCTTGATTAAGTGGGATTTAA 1641
DB 40 GGGAGCTTGATTAAGTGGGATTTAA 15

```

RESULT 7

AAL06791/C

ID AAL06791 standard; DNA; 31140 BP.

AC AAL06791;

XX

DT 21-NOV-2001 (first entry)

DE Human reproductive system related antigen DNA SEQ ID NO: 9479.

XX

KW Human; reproductive system related antigen; reproductive system disorder;

KW cancer; gene therapy; ds.

XX

OS Homo sapiens.

PN WO200155320-A2.

XX

PD 02-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US001339.

XX

PR 31-JAN-2000; 2000US-0179065P.

XX

PR 04-FEB-2000; 2000US-0180628P.

XX

PR 24-FEB-2000; 2000US-0184664P.

XX

PR 02-MAR-2000; 2000US-0186350P.

XX

PR 16-MAR-2000; 2000US-0189874P.

XX

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214885P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226273P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227109P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
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PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
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PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0233080P.
PR 08-SEP-2000; 2000US-0233081P.
PR 12-SEP-2000; 2000US-0233968P.
PR 14-SEP-2000; 2000US-023397P.
PR 14-SEP-2000; 2000US-023398P.
PR 14-SEP-2000; 2000US-023399P.
PR 14-SEP-2000; 2000US-023399P.
PR 14-SEP-2000; 2000US-023400P.
PR 14-SEP-2000; 2000US-023401P.
PR 14-SEP-2000; 2000US-0235063P.
PR 14-SEP-2000; 2000US-0235064P.
PR 14-SEP-2000; 2000US-0235065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0234984P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246476P.
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PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249267P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 06-DEC-2000; 2000US-0251866P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-465570/50.
Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
Disclousre; SEQ ID NO 9479; 1297pp + Sequence Listing; English.
The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a

CC protein of the invention
XX
SQ Sequence 31140 BP; 7333 A; 7322 C; 7497 G; 8988 T; 0 U; 0 Other;
Query Match 1.2%; Score 20; DB 4; Length 31140;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 534 TGAACGCTTTAAACTCC 553
DB 25120 TGAACGCTTTAAACTCC 25101
RESULT 8
ABA08065/c
ID ABA08065 standard; DNA; 31140 BP.
XX
AC ABA08065;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 860.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KM antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KM vulnerary; anticonvulsant; antibacterial; antitumoral; antiparasitic;
KM cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein; de.
XX
OS Homo sapiens.
XX
PN WO200155325-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001345.
XX
PR 31-JAN-2000; 2000US-0179065F.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0218290P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233065P.
PR 14-SEP-2000; 2000US-0233066P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241826P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246529P.
PR 08-NOV-2000; 2000US-0246602P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251858P.
 PR 08-DEC-2000; 2000US-0251859P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 XX (HUMA-) HUMAN GENOME SCT INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-488786/53.
 DR
 XX New isolated ovarian and/or breast cancer related nucleic acids and
 FT polypeptides, useful for diagnosing, treating and/or preventing human
 PT diseases and disorders, particularly ovarian and/or breast cancer.
 PS
 XX Disclosure: SEQ ID NO 860, 577bp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABA07454-ABA08224) and proteins
 CC (ABBI0743-ABBI0980) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 CC / (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 31140 BP; 7333 A; 7322 C; 7497 G; 8988 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20; DB 4; Length 31140;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 534 TGAAGCTGCTTTAAACTCC 553
 |||||
 |||||
 Db 25120 TGAAGCTGCTTTAAACTCC 25101
 |||||
 |||||
 RESULT 9
 AAD58279
 ID AAD58279 standard; DNA; 226475 BP.
 XX

AC AAD58279;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human tumour suppressor gene, lmt reverse complement DNA.
 XX
 KM Tumour suppressor gene; lmt; cancer; therapy; cytostatic; human; ds.
 XX
 OS Homo sapiens.
 XX
 FN WO2003066869-A1.
 XX
 PD 14-AUG-2003.
 XX
 PD 07-FEB-2003; 2003WO-AU000126.
 XX
 PF 07-FEB-2002; 2002AU-00000371.
 XX
 PR (HALL-) HALL INSTR MEDICAL RES WALTER & ELIZA.
 XX
 PA Cook WD, Mccaw BJ;
 XX
 PI WPI; 2003-646311/61.
 XX
 DR New nucleic acid molecule, useful for screening a subject for the
 PT presence of an aberration in a gene encoding an LMT.
 XX
 PS Claim 10; Page 233-299; 373pp; English.
 XX
 CC The invention relates to novel tumour suppressor gene, referred to as
 CC lmt. The invention also relates to the field of cancer therapy and cancer
 CC diagnostics. The nucleic acid molecule is useful for screening a subject
 CC for the presence of an aberration in a gene encoding an LMT. The present
 CC sequence is human lmt reverse complement DNA
 XX
 SQ Sequence 226475 BP; 61024 A; 41761 C; 40916 G; 57494 T; 0 U; 25280 Other;
 Query Match 1.2%; Score 20; DB 9; Length 226475;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 429 TGGTATGAGCAACCAATGCA 448
 |||||
 |||||
 Db 95864 TGGTATGAGCAACCAATGCA 95863
 |||||
 |||||
 RESULT 10
 AAA42733/C
 ID AAA42733 standard; CDNA; 407 BP.
 XX
 AC AAA42733;
 XX
 DT 21-AUG-2000 (first entry)
 XX
 DE Human secreted expressed sequence tag SEQ ID NO:1473.
 XX
 KM Human; mouse; xenopus; rat; secreted expressed sequence tag; SEST;
 KM expressed sequence tag; EST; probe; chemotactic; proliferative;
 KM immunomodulatory; haemotopoietic; chemokinetic; analgesic; haemostatic;
 KM thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
 KM antiviral; antidiabetic; antisthmatic; vulnerary; antiparkinsonian;
 KM anticancer; osteopathic; neuroprotective; nootropic; antipsoriatric;
 KM cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine;
 KM autoimmune disorder; multiple sclerosis; allergic condition;
 KM insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
 KM lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
 KM central nervous system disorder; Alzheimer's disease; stroke;
 KM Parkinson's disease; Huntington's disease; coagulation disorder;
 KM haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour;
 KM infection; depression; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX

PM WO20021990-A1.
 PD 20-APR-2000.
 XX 15-OCT-1999; 99WO-US024205.
 PF 15-OCT-1998; 98US-0104435P.
 PR 15-OCT-1998; 98US-0104435P.
 XX (GENY) GENETICS INST INC.
 PA Jacoba K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M,
 XX WPI: 2000-317937/27.
 DR
 XX Isolated polynucleotides, and encoded proteins, comprising secreted
 PT expressed sequence tags (sESTs), useful for treating various disorders
 PT such as autoimmune, infectious, and central nervous system disorders.
 XX
 PS Claim 1; Page 468-469; 618pp; English.
 XX
 CC AAA1261 to AAA43419 represent specifically claimed secreted expressed
 CC sequence tags (sESTs), isolated from human, mouse, xenopus and rat tissue
 CC sources. The sESTs can have a range of activities depending on the
 CC tissues they were isolated from. The activities include: chemotactic;
 CC proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
 CC haemostatic; thrombolytic; antiinflammatory; cyostatic; antibacterial;
 CC antifungal; antiviral; antidiabetic; antiasthmatic; vulnery; antileuc;
 CC osteoprotective; neuroprotective; nocotropic; antiparkinsonian; antipsoriatic;
 CC cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be
 CC used for gene therapy and in vaccines. The sESTs are useful as probes for
 CC the identification and isolation of full-length cDNAs and genomic DNA
 CC molecules which correspond to the sESTs. Proteins encoded by the sESTs
 CC are useful in assays for determining biological activity and raising
 CC antibodies. They may be useful for treatment of autoimmune disorders
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
 CC osteoporosis, osteoarthritis, central nervous system disorders
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
 CC disease), tumour, bacterial, fungal or viral infections, depression and
 CC psoriasis. AAA43420 to AAA43425 represent linker variants which are given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 407 BP; 131 A; 94 C; 126 G; 56 T; 0 U; 0 Other;
 Query Match 1.2%; Score 19; DB 3; Length 407;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 703 CTTCTTGTTCTGTGAGG 721
 |||||
 DB 398 CTTCTTGTTCTGTGAGG 380

RESULT 11
 ABA08624/C
 ID ABA08624 standard; cDNA; 453 BP.
 XX
 AC ABA08624;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human secreted protein homologue-encoding cDNA, SEQ ID NO:400.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemokines; chemokinesis; thrombolytic; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;

KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiaesthetic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cyostatic; osteopathic; vasotropic; cardiant; vitrucide; antibacterial;
 KW antifungal; vulnery; antileuc; ss.
 XX
 OS Homo sapiens.
 XX
 PM WO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Dmanac RT;
 XX
 DR WPI: 2001-457740/49.
 DR P-PSDB; ABB11380.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 1; Page 483; 1963pp; English.
 XX
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic; thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a cDNA encoding a
 CC novel human polypeptide of the invention
 XX
 SQ Sequence 453 BP; 124 A; 112 C; 139 G; 78 T; 0 U; 0 Other;
 Query Match 1.2%; Score 19; DB 4; Length 453;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 703 CTTCTGTTCTGTTGAGG 721
|||||
Db 187 CTTCTGTTCTGTTGAGG 169

RESULT 12
ID ADC32511/c
ID ADC32511 standard; cDNA; 453 BP.

AC ADC32511,
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Human novel cDNA contig sequence, SEQ ID NO:2593.
DE
XX
XX Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; antianemic; anticoagulant; thrombolytic; vulnerary;
KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy; chromosome 3; 88.
XX
XX Homo sapiens.
OS
XX
XX MO2003029271-A2.
PN
XX
XX 10-APR-2003.
PD
XX
XX 24-SEP-2002; 2002MO-US030474.
PF
XX
XX 24-SEP-2001; 2001US-0324631P.
PR
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou P, Ghosh M, Wang D, Ma Y, Aundi V, Wang Z, Weng G;
PI Haley-Vicente D, Dmanac RT;
PI
XX
XX WPI; 2003-371981/35.
DR P-PSDB; ADC33278.
DR
XX
XX New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anaemia, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
XX
XX Example 2; SEQ ID NO 2593; 1185bp; English.

CC The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's

CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a human contig
CC sequence used in an example of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 453 BP; 124 A; 112 C; 139 G; 78 T; 0 U; 0 Other;
Query Match 1.2%; Score 19; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 703 CTTCTGTTCTGTTGAGG 721
|||||
Db 187 CTTCTGTTCTGTTGAGG 169

RESULT 13
ID AAC76568/c
ID AAC76568 standard; cDNA; 909 BP.
XX
XX AAC76568;
AC
XX
XX 08-FEB-2001 (first entry)
DT
XX
XX Human ORF2123 polynucleotide sequence; SEQ ID NO:4245.
DE
XX
XX Human; open reading frame; ORF; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antineumatic; antihypertensive;
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; 88.
XX
XX Homo sapiens.
OS
XX
XX MO2000058473-A2.
PN
XX
XX 05-OCT-2000.
PD
XX
XX 31-MAR-2000; 2000MO-US008621.
PF
XX
XX 31-MAR-1999; 99US-0127607P.
PR 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
PR 30-MAR-2000; 2000US-00540763.
PA
XX
XX (CURA-) CURAGEN CORP.
PI
XX
XX Shimkets RA, Leach M;
PI
XX WPI; 2000-602362/57.
DR P-PSDB; AAB42359.
DR
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
XX Claim 5; Page 3441; 5507bp; English.

CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORF open reading frames 1 to 3161. The ORF
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antiproliferative; antiparkinsonian; neurotrophic; neuroprotective; osteopathic;
 CC anticonvulsant; antirheumatic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC demarcolytic; immunosuppressive; antineoplastic; antibacterial;
 CC antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORF-associated disorder. The nucleic acids may be used to express ORF
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive

CC Sequence 909 BP; 256 A; 236 C; 275 G; 141 T; 0 U; 1 Other;

CC Query Match 1.2%; Score 19; DB 3; Length 909;

CC Best Local Similarity 100.0%; Pred. No. 72;

CC Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 703 CTTCTTGCTTCTGTGAGG 721

CC 444 CTTCTTGCTTCTGTGAGG 426

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PT cancer.

XX Claim 1; SEQ ID NO 822; 1185bp; English.

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PT The invention relates to 971 novel human cDNA sequences (ADC29919-
 XX ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
 XX invention also relates to nucleic acid sequences over 99% identical with
 XX the novel human cDNAs. The invention additionally encompasses expression
 XX vectors and host cells comprising a nucleic acid of the invention; the
 XX recombinant production of a polypeptide of the invention; an antibody
 XX against a polypeptide of the invention; a method of detecting
 XX polynucleotides or polypeptides of the invention; and methods of
 XX identifying a compound which binds to a polypeptide of the invention. The
 XX invention further discloses methods of preventing, treating or
 XX ameliorating a medical condition; kits comprising polynucleotide probes
 XX and/or monoclonal antibodies for carrying out the methods of the
 XX invention; methods for the identification of compounds that modulate the
 XX expression or activity of the polynucleotide and/or polypeptide; and 767
 XX cDNA sequences corresponding to the cDNA sequences of the invention
 XX (ADC31861-ADC32627) and the polypeptides encoded by the cDNAs (ADC32628
 XX -ADC33394). The nucleic acids and polypeptides of the invention are
 XX useful in diagnostics, drug screening, forensics, gene mapping, in the
 XX identification of mutations responsible for genetic disorders or other
 XX traits, for assessing biodiversity, and in producing many other types of
 XX data and products dependent on DNA and amino acid sequences. They are
 XX also used for treating diseases such as Parkinson's disease, Alzheimer's
 XX disease and other neurodegenerative diseases, anaemia, platelet
 XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 XX cancer. The nucleic acids may also be used as hybridisation probes or
 XX primers, and in the recombinant production of a protein. The polypeptides
 XX are also useful in generating antibodies, as molecular weight markers,
 XX and as food supplements. The present sequence represents a specifically
 XX claimed human cDNA sequence of the invention. Note: The sequence data for
 XX this patent did not form part of the printed publication, but was
 XX obtained in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 1468 BP; 375 A; 389 C; 396 G; 308 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 19; DB 10; Length 1468;

XX Best Local Similarity 100.0%; Pred. No. 73;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 703 CTTCTTGCTTCTGTGAGG 721

XX 386 CTTCTTGCTTCTGTGAGG 368

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PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX MPI: 2003-029926/02.
DR P-PSDB; ABU17720.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

PS Claim 14; SEQ ID NO 9460; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1584 BP; 527 A; 307 C; 307 G; 443 T; 0 U; 0 Other;

XX Query Match 1.2%; Score 19; DB 8; Length 1584;

XX Best Local Similarity 100.0%; Pred. No. 73;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 591 TAATATGCTTCAGATAC 609

DB 1564 TAATATGCTTCAGATAC 1546

Search completed: November 9, 2004, 04:47:07
Job time : 890 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 9, 2004, 04:34:42 ; Search time 5405 Seconds
(without alignment)
11063.386 Million cell updates/sec

Title: US-09-651-651-4
Perfect score: 1641
Sequence: 1 atggagagcgaattcgaattc.....ctgataaagtgggacttaa 1641

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST:
1: gb_ecc1.*
2: gb_ecc2.*
3: gb_hcc.*
4: gb_ecc3.*
5: gb_ecc4.*
6: gb_ecc5.*
7: gb_ecc6.*
8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	410	25.0	596	1 AU237072	AU237072 AU237072
2	65	4.0	625	8 BH944186	BH944186 ch90a02.
3	58	3.5	546	9 CC948085	CC948085 BOHFI2TR
4	57	3.5	249	9 AU589191	AU589191 Arabidops
5	57	3.5	703	8 B2082259	B2082259 lkv30d04.
6	47	2.9	673	8 BH974466	BH974466 cd106g04.
7	40	2.4	40	8 BH864615	BH864615 SALK_0963
8	33	2.0	70	8 BH847141	BH847141 SALK_0134
9	32	2.0	207	8 BH746163	BH746163 g078e11.b
10	30	1.8	728	1 AU306500	AU306500 AU306500
11	29	1.8	303	8 BH548609	BH548609 BOHCO62TF
12	28	1.7	1225	8 B11175	B11175 F14L4-Sp6 I
13	24	1.5	632	4 B1922233	B1922233 EST542136
14	24	1.5	704	4 B1422757	B1422757 EST531423
15	24	1.5	788	7 CK259393	CK259393 EST705471
16	24	1.5	946	7 CK259394	CK259394 EST705472
17	23	1.4	251	7 CN770731	CN770731 taef2607.
18	23	1.4	382	8 B2763393	B2763393 SALK_1170
19	23	1.4	560	6 CD710878	CD710878 VVA026C02
20	23	1.4	565	5 B0584361	B0584361 E011859-0
21	22	1.3	556	9 C1588639	C1588639 OR_Ba008
22	22	1.3	651	9 C8521850	C8521850 t1gr-g8a-
23	22	1.3	690	4 BG703033	BG703033 602685844
24	22	1.3	912	4 BG180774	BG180774 602327188

C 25	21	1.3	493	9 CC948076	CC948076 BOHFI2TF
C 26	21	1.3	502	7 CK115712	CK115712 Y014D01 P
C 27	20	1.2	191	2 AM057143	AM057143 ca01d02.y
C 28	20	1.2	240	6 C70865	C70865 C70865 Yxji
C 29	20	1.2	303	2 BB495738	BB495738 BB495738
C 30	20	1.2	306	2 BF847741	BF847741 ILS-EN008
C 31	20	1.2	325	2 BB492868	BB492868 BB492868
C 32	20	1.2	360	1 AV201222	AV201222 AV201222
C 33	20	1.2	360	1 AV203275	AV203275 AV203275
C 34	20	1.2	360	6 C67741	C67741 C67741 Yxji
C 35	20	1.2	360	6 C69687	C69687 C69687 Yxji
C 36	20	1.2	383	6 C70548	C70548 C70548 Yxji
C 37	20	1.2	389	8 BH451075	BH451075 BOHFO84TF
C 38	20	1.2	427	8 AQ198065	AQ198065 RPI11-46
C 39	20	1.2	428	4 B1759121	B1759121 B1759121
C 40	20	1.2	431	8 A0564754	A0564754 HS_5361 A
C 41	20	1.2	434	1 AV914566	AV914566 AV914566
C 42	20	1.2	478	7 CK581181	CK581181 IST_WIS-3
C 43	20	1.2	483	8 AQ493090	AQ493090 HS_5211_B
C 44	20	1.2	503	8 AQ195384	AQ195384 RPI11-46
C 45	20	1.2	504	5 BU972434	BU972434 HB21K04r
C 46	20	1.2	521	2 BF054499	BF054499 EST439729
C 47	20	1.2	553	4 B1468114	B1468114 ESTD0521
C 48	20	1.2	565	8 AQ372820	AQ372820 RPI11-15
C 49	20	1.2	570	8 BH107520	BH107520 RPI1-24-3
C 50	20	1.2	573	6 CA500577	CA500577 WHE4021_F
C 51	20	1.2	574	1 AV835512	AV835512 AV835512
C 52	20	1.2	578	5 BX301173	BX301173 BX301173
C 53	20	1.2	591	2 BF587570	BF587570 FMI_38_A0
C 54	20	1.2	599	2 AM036854	AM036854 614019F11
C 55	20	1.2	608	2 BF338987	BF338987 602036062
C 56	20	1.2	638	5 BQ471308	BQ471308 HV02A09r
C 57	20	1.2	644	1 AV913458	AV913458 AV913458
C 58	20	1.2	665	6 CD900920	CD900920 G356_102D
C 59	20	1.2	666	8 BH974706	BH974706 cd106g04.
C 60	20	1.2	686	5 BQ508623	BQ508623 EST1618038
C 61	20	1.2	690	4 B1235635	B1235635 B1235635
C 62	20	1.2	697	4 B1177423	B1177423 EST518368
C 63	20	1.2	703	9 CG449358	CG449358 OG7AB05TH
C 64	20	1.2	703	1 CG450012	CG450012 OG7AB06TV
C 65	20	1.2	713	1 A1611143	A1611143 A1611143
C 66	20	1.2	756	9 BX217764	BX217764 Danilo rer
C 67	20	1.2	763	9 CC560623	CC560623 CH240_470
C 68	20	1.2	792	4 BG600021	BG600021 EST504916
C 69	20	1.2	838	8 B12295	B12295 T20ms-Sp6 T
C 70	20	1.2	848	3 AY108921	AY108921 Zea mays
C 71	20	1.2	889	3 CG955720	CG955720 MBEM83TR
C 72	20	1.2	890	6 CD325432	CD325432 AGENCOURT
C 73	20	1.2	931	9 CG921778	CG921778 MBH131TR
C 74	20	1.2	959	9 CC718562	CC718562 OGJDM33TH
C 75	20	1.2	968	7 CK260764	CK260764 EST706842
C 76	20	1.2	1002	8 A2672942	A2672942 ENT1V5TF
C 77	20	1.2	1021	4 BG281245	BG281245 602401706
C 78	20	1.2	1030	9 CL052427	CL052427 CH216-75N
C 79	20	1.2	1073	7 CK212372	CK212372 FGAS02424
C 80	20	1.2	113	3 AK085217	AK085217 Mue muscu
C 81	19	1.2	113	8 B2383343	B2383343 SALK_1324
C 82	19	1.2	189	5 BU917428	BU917428 JKO4B05 S
C 83	19	1.2	217	2 BB029739	BB029739 BB029739
C 84	19	1.2	225	1 AV367815	AV367815 AV367815
C 85	19	1.2	229	1 AL599448	AL599448 DKFZP313N
C 86	19	1.2	259	7 CN556474	CN556474 taeg37a11.
C 87	19	1.2	267	1 AA638182	AA638182 v196b04.x
C 88	19	1.2	283	2 BB160755	BB160755 BB160755
C 89	19	1.2	283	2 BB351789	BB351789 BB351789
C 90	19	1.2	306	6 CD181201	CD181201 WSI_-0030T
C 91	19	1.2	309	1 AV051299	AV051299 AV051299
C 92	19	1.2	309	2 BB498764	BB498764 BB498764
C 93	19	1.2	310	1 AV277827	AV277827 AV277827
C 94	19	1.2	311	6 CD553419	CD553419 B0359D11-
C 95	19	1.2	314	6 CD554265	CD554265 B0373811-
C 96	19	1.2	318	2 BB167702	BB167702 BB167702
C 97	19	1.2	318	2 BB341313	BB341313 BB341313

C 98	19	1.2	318	2	BB491357	BB491357	BB491337	C 171	19	1.2	674	9	CR425314	CR425314	CR425314	tiGr-988-
99	19	1.2	325	2	BB218348	BB218348	BB218348	172	19	1.2	675	4	BG449977	BG449977	BG449977	BM012D06D
100	19	1.2	343	4	BB454495	BB454495	BB454495	173	19	1.2	676	8	AZ789485	AZ789485	AZ789485	2M0037K13
101	19	1.2	346	7	CR466415	CR466415	CR466415	C 174	19	1.2	677	4	BI309412	BI309412	BI309412	EST530822
102	19	1.2	360	5	BY380442	BY380442	BY380442	175	19	1.2	678	2	BB200448	BB200448	BB200448	BB200448
C 103	19	1.2	383	9	CC929527	CC929527	ZMBBC053	176	19	1.2	681	6	CB488869	CB488869	CB488869	CMYKrc4h0
C 104	19	1.2	405	1	AI115594	AI115594	unH7e04.r	177	19	1.2	689	1	AI065163	AI065163	AI065163	HA1005.Hu
C 105	19	1.2	415	2	BF715659	BF715659	mab10b09.r	178	19	1.2	699	5	BQ863393	BQ863393	BQ863393	QGC23W06.
C 106	19	1.2	426	7	H56980	H56980	yT07a03.r.1	179	19	1.2	699	5	BX310965	BX310965	BX310965	BM8110965
C 107	19	1.2	429	1	AU267362	AU267362	AU267362	C 180	19	1.2	701	5	BH871322	BH871322	BH871322	Q028C09.P
108	19	1.2	434	2	BB750671	BB750671	BB750671	181	19	1.2	702	8	B2105069	B2105069	B2105069	CH230-227
109	19	1.2	436	7	CK096173	CK096173	UA50BPC12	C 182	19	1.2	702	8	CC786947	CC786947	CC786947	ZMMBB015
110	19	1.2	439	2	AM053755	AM053755	L30--1648T	C 183	19	1.2	703	9	CE552010	CE552010	CE552010	tiGr-988-
111	19	1.2	440	1	AA896937	AA896937	L30--369T3	C 184	19	1.2	712	9	AG329124	AG329124	AG329124	Mus.mbcu
C 112	19	1.2	443	8	AZ259430	AZ259430	RPCT-23-1	185	19	1.2	723	9	AG393024	AG393024	AG393024	Mus.mbcu
113	19	1.2	466	7	CM465987	CM465987	LCB002D16	186	19	1.2	724	8	BH422051	BH422051	BH422051	BOHNPTOTR
114	19	1.2	468	1	AA856218	AA856218	L30--239T3	187	19	1.2	726	4	BG921389	BG921389	BG921389	602824256
C 115	19	1.2	471	8	AZ163210	AZ163210	SP.0073.A	188	19	1.2	733	9	CG682692	CG682692	CG682692	ZMMBB-C015
C 116	19	1.2	472	5	B0820015	B0820015	UA50BPC12	189	19	1.2	735	7	CK636205	CK636205	CK636205	UT-M-HN0-
C 117	19	1.2	475	8	B2120282	B2120282	CH230-264	190	19	1.2	752	2	BE916493	BE916493	BE916493	601667068
118	19	1.2	476	1	AA154747	AA154747	mc64e03.r	191	19	1.2	754	4	BI558629	BI558629	BI558629	603240636
119	19	1.2	476	1	AA154747	AA154747	mc64e03.r	192	19	1.2	756	8	AQ919963	AQ919963	AQ919963	RPCT-23-2
C 120	19	1.2	476	9	AG227482	AG227482	Lotus.cor	193	19	1.2	758	9	AG540973	AG540973	AG540973	Mus.mbcu
121	19	1.2	482	8	BH004158	BH004158	BMBXC0710	194	19	1.2	761	8	BH455377	BH455377	BH455377	BOGVOS8TR
C 122	19	1.2	486	8	BH184362	BH184362	025_G_12-	C 195	19	1.2	763	7	CO046417	CO046417	CO046417	UT-M-HU0-
C 123	19	1.2	486	9	CNS07PBK	CNS07PBK	AL621314	196	19	1.2	764	9	CL400513	CL400513	CL400513	ZMMBB039
C 124	19	1.2	509	4	BJ454333	BJ454333	T3 end of	C 197	19	1.2	769	8	B2077376	B2077376	B2077376	1Kx31C03.
C 125	19	1.2	510	6	CB487034	CB487034	CMYKrcdho	C 198	19	1.2	780	7	CN053715	CN053715	CN053715	Salamanca
C 126	19	1.2	513	6	CA990677	CA990677	EST644185	C 199	19	1.2	784	5	BU283961	BU283961	BU283961	603862865
127	19	1.2	515	5	BU761169	BU761169	aa664a12.	C 200	19	1.2	798	4	BG584891	BG584891	BG584891	EST486652
C 128	19	1.2	517	7	CK106007	CK106007	UA50BPC12	C 201	19	1.2	806	9	CG675565	CG675565	CG675565	tr83297.T
C 129	19	1.2	520	6	CA355869	CA355869	627850.NC	202	19	1.2	808	8	B2435706	B2435706	B2435706	BONNU12TF
C 130	19	1.2	521	8	AO835756	AO835756	HS.4674.A	C 203	19	1.2	813	6	CA922278	CA922278	CA922278	EST639996
C 131	19	1.2	529	2	BB855462	BB855462	BB855462	C 204	19	1.2	817	9	CG919282	CG919282	CG919282	MBEAT07TR
C 132	19	1.2	529	5	BK524700	BK524700	BK524700	205	19	1.2	820	5	BX927594	BX927594	BX927594	BK927594
C 133	19	1.2	537	1	AT505267	AT505267	vp97f12.x	206	19	1.2	821	9	CL140900	CL140900	CL140900	ISB1-118B
C 134	19	1.2	537	9	CC902352	CC902352	ZMMBB024	207	19	1.2	822	6	CA846248	CA846248	CA846248	haa11d09.
C 135	19	1.2	543	2	AM935968	AM935968	QV3-DT001	C 208	19	1.2	837	2	BE642769	BE642769	BE642769	Cx12.6_P0
C 136	19	1.2	543	6	CF164602	CF164602	B0745C03-	C 209	19	1.2	843	2	BF623020	BF623020	BF623020	HVSEa001
137	19	1.2	550	4	BG088851	BG088851	h3158D07-	210	19	1.2	856	4	BI659584	BI659584	BI659584	603303137
C 138	19	1.2	553	2	BB853020	BB853020	un28d11.x	211	19	1.2	875	9	CG919226	CG919226	CG919226	MBEBH2CTF
139	19	1.2	553	4	BG246682	BG246682	602360740	212	19	1.2	878	5	B0733857	B0733857	B0733857	AGENCOURT
140	19	1.2	558	2	BE116922	BE116922	UI-R-BB1-	C 213	19	1.2	891	5	B0433760	B0433760	B0433760	AGENCOURT
141	19	1.2	568	4	BI774098	BI774098	466076.MA	C 214	19	1.2	893	1	AA203733	AA203733	AA203733	zx53h04.r
142	19	1.2	573	8	AZ232370	AZ232370	RPCT-23-6	C 215	19	1.2	903	8	CC125140	CC125140	CC125140	NDL.78J23
143	19	1.2	581	2	AM973353	AM973353	EST385496	C 216	19	1.2	912	9	CC875163	CC875163	CC875163	HSC.00701
144	19	1.2	584	6	CA340901	CA340901	haa73c02.	C 217	19	1.2	915	5	BQ135466	BQ135466	BQ135466	NFO06F07B
145	19	1.2	584	6	CF163855	CF163855	B0734A05-	218	19	1.2	916	8	CC143740	CC143740	CC143740	NDL.18r12
146	19	1.2	604	9	CR315959	CR315959	Medicago	219	19	1.2	920	2	BE794531	BE794531	BE794531	601590285
C 147	19	1.2	609	5	BQ826913	BQ826913	gd49a11.x	220	19	1.2	932	7	CN645048	CN645048	CN645048	ILLUMIGEN
148	19	1.2	609	7	CF917504	CF917504	BfL0r498.	221	19	1.2	935	2	BB614286	BB614286	BB614286	Ar6b1d286
149	19	1.2	611	4	BI383705	BI383705	BFLG2.001	C 222	19	1.2	936	3	CNS0A340	CNS0A340	CNS0A340	Ar6b1d286
150	19	1.2	614	1	AV909896	AV909896	AV909896	C 223	19	1.2	945	8	CC223500	CC223500	CC223500	CH261-105
151	19	1.2	617	5	BU814893	BU814893	N035H03.P	224	19	1.2	950	9	BF180992	BF180992	BF180992	601805038
C 152	19	1.2	619	1	AL596750	AL596750	DXF2p451D	225	19	1.2	964	9	CNS02V08	CNS02V08	CNS02V08	Tetradon
153	19	1.2	619	2	BF024794	BF024794	gd1ld10.Y	226	19	1.2	972	6	BY711192	BY711192	BY711192	BY711192
154	19	1.2	623	8	BZ271453	BZ271453	CH230-410	C 227	19	1.2	972	9	CL471665	CL471665	CL471665	SALT.164
155	19	1.2	630	6	CD770392	CD770392	AGENCOURT	C 228	19	1.2	990	5	BU504817	BU504817	BU504817	AGENCOURT
C 156	19	1.2	631	6	CB246853	CB246853	UI-M-F10-	C 229	19	1.2	994	2	BB613522	BB613522	BB613522	601504278
157	19	1.2	631	6	CD771359	CD771359	AGENCOURT	C 230	19	1.2	1021	9	CL114127	CL114127	CL114127	ISB1-59K2
C 158	19	1.2	634	9	CE615147	CE615147	tiGr-988-	231	19	1.2	1052	3	AK029452	AK029452	AK029452	Mus.mbcu
C 159	19	1.2	636	6	CF232420	CF232420	PtaUX001	232	19	1.2	1111	3	AK040295	AK040295	AK040295	Mus.mbcu
160	19	1.2	637	6	AO814411	AO814411	HS.5511.B	C 233	19	1.2	1113	8	B2562981	B2562981	B2562981	pac82-164
C 161	19	1.2	643	6	CA380888	CA380888	660286.NC	C 234	19	1.2	1130	8	B2578287	B2578287	B2578287	m8r2.5773
C 162	19	1.2	643	5	BO584761	BO584761	E011262-0	C 235	19	1.2	1238	8	BH770371	BH770371	BH770371	ILMGfAg14
C 163	19	1.2	647	5	BB832766	BB832766	T038A04.P	236	19	1.2	1344	2	BF577525	BF577525	BF577525	602092378
C 164	19	1.2	648	6	BY26789	BY26789	BY26789	237	19	1.2	1325	3	AK011996	AK011996	AK011996	Mus.mbcu
165	19	1.2	655	9	CR485220	CR485220	Medicago	238	19	1.2	1353	3	AK079056	AK079056	AK079056	Mus.mbcu
166	19	1.2	658	6	CB515588	CB515588	MSP0033	C 239	18	1.1	180	1	AA783081	AA783081	AA783081	a5d09a1.f
167	19	1.2	659	9	BX123534	BX123534	Danio.ref	C 240	18	1.1	216	8	AZ889109	AZ889109	AZ889109	RPCT-24-1
C 168	19	1.2	661	5	BU893991	BU893991	P085F02.P	C 241	18	1.1	218	2	BE159187	BE159187	BE159187	MRO-HT040
C 169	19	1.2	662	5	BU251577	BU251577	603402768	C 242	18	1.1	220	1	AA169312	AA169312	AA169312	zp20606.r
170	19	1.2	674	2	BB207669	BB207669	BB207669	C 243	18	1.1	221	6	CD492298	CD492298	CD492298	DD6-87B.D

C 244	18	1.1	221	7	CR581072	C 317	18	1.1	336	7	CK579958
C 245	18	1.1	223	9	CG10218	C 319	18	1.1	397	2	BF013824
C 246	18	1.1	224	8	A0531687	C 318	18	1.1	397	2	CC602321
C 247	18	1.1	227	7	CR581074	C 320	18	1.1	398	6	BY691704
C 248	18	1.1	231	9	CG786555	C 321	18	1.1	399	9	CC929862
C 249	18	1.1	238	9	CL239137	C 322	18	1.1	403	2	BB820954
C 250	18	1.1	239	1	A1151937	C 323	18	1.1	404	8	B2708056
C 251	18	1.1	239	1	AA410532	C 324	18	1.1	405	2	AW733457
C 252	18	1.1	241	4	BM151497	C 325	18	1.1	406	1	AA785018
C 253	18	1.1	249	4	CR390107	C 326	18	1.1	409	4	B6652434
C 254	18	1.1	255	4	BI403556	C 327	18	1.1	411	2	BE024012
C 255	18	1.1	258	1	A1867614	C 328	18	1.1	414	4	B614684
C 256	18	1.1	260	7	CR581075	C 329	18	1.1	414	8	AQ106506
C 257	18	1.1	261	7	CR581073	C 330	18	1.1	415	2	BF595358
C 258	18	1.1	262	1	AA303749	C 331	18	1.1	416	1	AU284193
C 259	18	1.1	265	2	BB565597	C 332	18	1.1	416	5	BX279797
C 260	18	1.1	265	2	CR854847	C 333	18	1.1	418	4	BG882817
C 261	18	1.1	268	2	AW783719	C 334	18	1.1	418	9	CL003739
C 262	18	1.1	272	7	CK987737	C 335	18	1.1	422	2	AW457854
C 263	18	1.1	284	2	BB741048	C 336	18	1.1	425	6	CD178945
C 264	18	1.1	284	4	BI177887	C 337	18	1.1	428	2	AW504350
C 265	18	1.1	287	4	BB313214	C 338	18	1.1	428	6	CB094320
C 266	18	1.1	293	8	AQ684988	C 339	18	1.1	428	7	N40274
C 267	18	1.1	294	8	A2909584	C 340	18	1.1	431	4	BI815066
C 268	18	1.1	295	2	AW856166	C 341	18	1.1	431	4	BM689921
C 269	18	1.1	301	7	W12301	C 342	18	1.1	432	2	BE566130
C 270	18	1.1	301	7	W12301	C 343	18	1.1	434	2	AM028752
C 271	18	1.1	304	8	BZ708067	C 344	18	1.1	434	5	BQ863085
C 272	18	1.1	306	1	AJ670617	C 345	18	1.1	434	1	AJ648090
C 273	18	1.1	311	1	AV827958	C 346	18	1.1	436	1	AJ648090
C 274	18	1.1	316	2	BB271409	C 347	18	1.1	437	6	CD992551
C 275	18	1.1	318	6	BI022005	C 348	18	1.1	437	7	R35440
C 276	18	1.1	318	6	CD073704	C 349	18	1.1	438	4	BM857145
C 277	18	1.1	319	9	CG824214	C 350	18	1.1	438	5	BQ694412
C 278	18	1.1	324	1	AJ497021	C 351	18	1.1	439	1	AJ655627
C 279	18	1.1	324	7	BI022010	C 352	18	1.1	439	2	BB815333
C 280	18	1.1	324	7	CK766729	C 353	18	1.1	439	8	AQ773481
C 281	18	1.1	332	2	BP814934	C 354	18	1.1	440	7	H46292
C 282	18	1.1	336	1	AV772113	C 355	18	1.1	441	1	AA930440
C 283	18	1.1	337	8	Z24989	C 356	18	1.1	442	9	CE541720
C 284	18	1.1	340	7	AQ104443	C 357	18	1.1	442	6	CD158541
C 285	18	1.1	341	7	N97698	C 358	18	1.1	446	9	TA125D07P
C 286	18	1.1	344	4	BJ215679	C 359	18	1.1	447	1	AJ791935
C 287	18	1.1	345	2	AW383522	C 360	18	1.1	447	6	CB746984
C 288	18	1.1	345	6	BY774937	C 361	18	1.1	447	7	CR547315
C 289	18	1.1	347	1	AV696774	C 362	18	1.1	447	8	AQ7064740
C 290	18	1.1	347	8	BZ107941	C 363	18	1.1	448	2	AM822068
C 291	18	1.1	348	1	CC811523	C 364	18	1.1	449	6	CD178585
C 292	18	1.1	348	1	A1213899	C 365	18	1.1	453	7	W95309
C 293	18	1.1	348	7	T34563	C 366	18	1.1	454	8	AQ674105
C 294	18	1.1	349	5	BO510059	C 367	18	1.1	456	2	BF423682
C 295	18	1.1	359	4	BD465223	C 368	18	1.1	457	8	AQ056241
C 296	18	1.1	360	6	CD144258	C 369	18	1.1	460	2	BE028794
C 297	18	1.1	360	8	B38290	C 370	18	1.1	461	4	BI432500
C 298	18	1.1	363	2	BE081644	C 371	18	1.1	461	4	BM404578
C 299	18	1.1	365	6	CA002004	C 372	18	1.1	461	6	CB737224
C 300	18	1.1	367	4	BT678512	C 373	18	1.1	462	4	BI403472
C 301	18	1.1	368	9	CE839709	C 374	18	1.1	462	6	CB159560
C 302	18	1.1	370	8	AQ261286	C 375	18	1.1	463	6	CD2476
C 303	18	1.1	371	6	CD190591	C 376	18	1.1	465	4	BI536390
C 304	18	1.1	371	9	CG701469	C 377	18	1.1	466	1	AA455642
C 305	18	1.1	374	8	AZ910802	C 378	18	1.1	467	6	CD22475
C 306	18	1.1	375	5	BY583614	C 379	18	1.1	470	2	BE120939
C 307	18	1.1	375	7	Z18066	C 380	18	1.1	471	6	CB732706
C 308	18	1.1	382	7	T10644	C 381	18	1.1	473	9	CG218941
C 309	18	1.1	386	4	BM698701	C 382	18	1.1	474	8	BZ371230
C 310	18	1.1	388	1	AA218702	C 383	18	1.1	475	2	BF977614
C 311	18	1.1	389	9	CC794687	C 384	18	1.1	477	1	AI607134
C 312	18	1.1	391	5	BU894286	C 385	18	1.1	477	1	AA168119
C 313	18	1.1	391	5	CG710221	C 386	18	1.1	478	5	BO506820
C 314	18	1.1	392	1	AV426830	C 387	18	1.1	479	4	BG596474
C 315	18	1.1	395	1	AL789130	C 388	18	1.1	479	4	CC161969
C 316	18	1.1	395	9	CG398021	C 389	18	1.1	480	8	BH754545

536	18	1.1	610	7	CR448952	609	18	1.1	657	5	BU487149
537	18	1.1	611	1	AL036362	610	18	1.1	658	5	BU488336
538	18	1.1	611	1	AG259200	611	18	1.1	658	5	CG622230
539	18	1.1	612	6	CB923780	612	18	1.1	659	8	BH271379
540	18	1.1	612	8	AQ238696	613	18	1.1	660	5	BO548523
541	18	1.1	613	8	DR228248	614	18	1.1	660	8	BH391979
542	18	1.1	613	9	CC698850	615	18	1.1	661	1	AL600911
543	18	1.1	614	9	CC698850	616	18	1.1	661	2	AL600911
544	18	1.1	614	9	BM726216	617	18	1.1	662	4	BM694986
545	18	1.1	615	4	CG338912	618	18	1.1	663	4	BM694986
546	18	1.1	615	6	CG338912	619	18	1.1	664	4	BM694986
547	18	1.1	617	4	CG338912	620	18	1.1	665	1	AL129912
548	18	1.1	618	6	CG338912	621	18	1.1	665	4	BM827891
549	18	1.1	619	7	CG338912	622	18	1.1	665	8	BH256769
550	18	1.1	620	4	BM816281	623	18	1.1	666	7	CR285990
551	18	1.1	620	4	BM816281	624	18	1.1	667	2	AM915530
552	18	1.1	620	8	AQ969653	625	18	1.1	667	5	BU487079
553	18	1.1	621	8	BM777573	626	18	1.1	667	5	BU487079
554	18	1.1	622	8	BM777573	627	18	1.1	669	4	BM728921
555	18	1.1	622	8	CG164253	628	18	1.1	669	4	BM860126
556	18	1.1	622	9	CG241006	629	18	1.1	673	4	CG432746
557	18	1.1	624	2	BM7287079	630	18	1.1	673	4	BM506738
558	18	1.1	626	2	BM192694	631	18	1.1	674	5	BU490871
559	18	1.1	629	2	AM961701	632	18	1.1	674	5	CE631033
560	18	1.1	629	4	BM104136	633	18	1.1	675	5	BU396366
561	18	1.1	630	4	BM104136	634	18	1.1	678	6	CA172751
562	18	1.1	631	1	AA138702	635	18	1.1	680	8	CG164252
563	18	1.1	631	9	CR506463	636	18	1.1	681	4	BM539624
564	18	1.1	631	9	CR506463	637	18	1.1	681	4	BM539624
565	18	1.1	632	5	BM869775	638	18	1.1	683	8	BZ31517
566	18	1.1	632	5	BM869775	639	18	1.1	684	9	CL661532
567	18	1.1	632	6	CG133822	640	18	1.1	685	4	BM736859
568	18	1.1	633	6	CG133822	641	18	1.1	685	7	CG541797
569	18	1.1	634	6	CA731063	642	18	1.1	685	1	AL1968234
570	18	1.1	634	8	BM815350	643	18	1.1	686	6	CG031133
571	18	1.1	634	8	BM815350	644	18	1.1	686	6	CG031133
572	18	1.1	636	2	BE080127	645	18	1.1	686	6	AG2973106
573	18	1.1	637	6	CF249426	646	18	1.1	686	8	BZ312767
574	18	1.1	639	4	BM492266	647	18	1.1	687	9	CG350049
575	18	1.1	639	6	CG675979	648	18	1.1	689	2	BE407729
576	18	1.1	640	2	AM992891	649	18	1.1	689	7	CG937952
577	18	1.1	640	5	BM160379	650	18	1.1	689	7	CG937952
578	18	1.1	641	8	CG561789	651	18	1.1	691	2	BE787707
579	18	1.1	644	8	BZ906825	652	18	1.1	691	5	BM938634
580	18	1.1	644	8	CG957667	653	18	1.1	691	5	BM938634
581	18	1.1	644	5	BM164633	654	18	1.1	693	5	BM938634
582	18	1.1	645	6	CA132978	655	18	1.1	693	6	BM938634
583	18	1.1	645	7	BM705334	656	18	1.1	694	5	BM938634
584	18	1.1	645	8	BM705334	657	18	1.1	694	5	BM938634
585	18	1.1	645	8	BM705334	658	18	1.1	694	5	BM938634
586	18	1.1	645	8	BM705334	659	18	1.1	694	5	BM938634
587	18	1.1	647	4	BM694768	660	18	1.1	695	4	BM938634
588	18	1.1	647	4	BM694768	661	18	1.1	695	4	BM938634
589	18	1.1	648	7	CG500814	662	18	1.1	697	5	BM938634
590	18	1.1	648	7	CG500814	663	18	1.1	697	7	CG500814
591	18	1.1	649	5	BM163888	664	18	1.1	697	7	CG500814
592	18	1.1	650	5	BM163888	665	18	1.1	698	8	CG500814
593	18	1.1	650	5	BM163888	666	18	1.1	698	8	CG500814
594	18	1.1	651	6	CG207749	667	18	1.1	699	8	CG500814
595	18	1.1	651	6	CG207749	668	18	1.1	699	8	CG500814
596	18	1.1	651	8	AG2440503	669	18	1.1	701	5	BM938634
597	18	1.1	652	4	BM1919186	670	18	1.1	701	5	BM938634
598	18	1.1	652	4	BM1919186	671	18	1.1	702	5	BM938634
599	18	1.1	653	1	BM1919186	672	18	1.1	702	5	BM938634
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601	18	1.1	653	5	BM1919186	674	18	1.1	703	7	CG817716
602	18	1.1	654	8	BM1919186	675	18	1.1	704	5	BM938634
603	18	1.1	654	8	BM1919186	676	18	1.1	704	5	BM938634
604	18	1.1	654	9	CG372743	677	18	1.1	704	4	AG345327
605	18	1.1	655	1	BM266512	678	18	1.1	706	5	BM938634
606	18	1.1	655	1	BM266512	679	18	1.1	706	5	BM938634
607	18	1.1	656	6	CG1332029	680	18	1.1	706	8	BM938634
608	18	1.1	656	8	AG823074	681	18	1.1	707	4	BM938634

662	18	1.1	707	8	BH967534	BH67534	cdj32d10.	755	18	1.1	745	9	CR342873	CR342873
C 663	18	1.1	707	8	BZ198574	BZ198574	CH230-270	C 756	18	1.1	745	9	CL188661	CL188661
C 684	18	1.1	708	7	CR844347	UI-R-BJ1-		C 757	18	1.1	746	9	AG579279	AG579279
685	18	1.1	708	9	CR051344	CR051344	Forward s	758	18	1.1	748	7	CR869636	CR869636
C 687	18	1.1	709	6	BU487467	BU487467	604124852	759	18	1.1	748	7	CN206877	CN206877
C 688	18	1.1	709	6	CR516136	CR516136	ssalrpb51	C 760	18	1.1	748	7	CN232583	CN232583
C 689	18	1.1	711	9	CR458056	CR458056	ligr-gss-	761	18	1.1	748	7	AG490663	AG490663
C 690	18	1.1	711	9	CG483741	CG483741	602503379	762	18	1.1	749	4	BS070734	BS070734
C 691	18	1.1	712	8	BH674678	BH674678	BOMAB287R	C 763	18	1.1	749	9	CC709181	CC709181
C 692	18	1.1	712	8	BX223222	BX223222	Danilo rer	764	18	1.1	750	5	B0863744	B0863744
C 693	18	1.1	713	9	CE129718	CE129718	ligr-gss-	C 765	18	1.1	750	7	CN077364	CN077364
C 694	18	1.1	713	9	CR024281	CR024281	AGENCOURT	766	18	1.1	751	5	BU416346	BU416346
C 695	18	1.1	713	7	CR339714	CR339714	CGF100474	C 767	18	1.1	751	7	CR554523	CR554523
C 696	18	1.1	715	5	BU486994	BU486994	604124804	C 768	18	1.1	751	7	CR579660	CR579660
C 697	18	1.1	716	2	BB367638	BB367638	BB367638	C 769	18	1.1	751	8	BZ774503	BZ774503
C 698	18	1.1	716	7	CO103472	CO103472	GR_Eb003	C 770	18	1.1	751	8	BZ959965	BZ959965
C 699	18	1.1	717	5	BU486692	BU486692	604127605	C 771	18	1.1	751	9	CC634249	CC634249
C 699	18	1.1	717	7	CK707398	CK707398	ZF101-P00	C 772	18	1.1	751	9	CU116908	CU116908
C 700	18	1.1	717	8	BZ921766	BZ921766	CH240_119	C 773	18	1.1	752	4	BU742816	BU742816
C 701	18	1.1	718	5	BU417494	BU417494	6036771503	C 774	18	1.1	752	5	BU486944	BU486944
C 702	18	1.1	719	7	CN057182	CN057182	Salamande	775	18	1.1	752	7	CN170561	CN170561
C 703	18	1.1	719	9	CN294479	CN294479	170005313	C 776	18	1.1	752	9	CC600200	CC600200
C 704	18	1.1	719	9	CE409861	CE409861	ligr-gss-	C 777	18	1.1	754	4	BU748649	BU748649
C 705	18	1.1	720	8	CN294463	CN294463	170005830	C 778	18	1.1	754	7	CR305986	CR305986
C 706	18	1.1	720	8	BZ227625	BZ227625	id29c12.g	C 779	18	1.1	754	7	CO117100	CO117100
C 707	18	1.1	720	9	CNS00K3A	AL094372	Arabidops	C 780	18	1.1	756	4	BI254863	BI254863
C 708	18	1.1	721	5	BX115485	BX115485	AX15485	C 781	18	1.1	756	9	CR319091	CR319091
C 709	18	1.1	721	7	CO074603	CO074603	GR_Ea34M	C 782	18	1.1	756	9	CL159606	CL159606
C 710	18	1.1	722	4	BU625447	BU625447	BU625447	C 783	18	1.1	757	9	CC610576	CC610576
C 711	18	1.1	722	5	BU417107	BU417107	6036771414	C 784	18	1.1	758	7	CR866690	CR866690
C 712	18	1.1	722	7	CR427981	CR427981	CR427981	C 785	18	1.1	759	7	BU492046	BU492046
C 713	18	1.1	724	5	BU488716	BU488716	604127187	C 786	18	1.1	759	7	CR868708	CR868708
C 714	18	1.1	725	5	BU932504	BU932504	AGENCOURT	C 787	18	1.1	760	8	BZ793280	BZ793280
C 715	18	1.1	725	6	CA429752	CA429752	UI-H-FH1-	C 788	18	1.1	760	8	CC611230	CC611230
C 716	18	1.1	726	9	CC723940	CC723940	OGVEP75TH	C 789	18	1.1	761	8	BZ973813	BZ973813
C 717	18	1.1	727	5	BU487236	BU487236	604127173	C 790	18	1.1	762	4	BG967183	BG967183
C 718	18	1.1	727	9	CC636397	CC636397	OGCDP56TC	C 791	18	1.1	762	7	CK025010	CK025010
C 719	18	1.1	728	6	BO865166	BO865166	OGC28021.	C 792	18	1.1	763	7	AL159882	AL159882
C 720	18	1.1	728	6	BY731748	BY731748	601122856	C 793	18	1.1	763	7	CK127633	CK127633
C 721	18	1.1	729	2	BE274857	BE274857	601122856	C 794	18	1.1	764	4	BI310207	BI310207
C 722	18	1.1	729	4	BM763262	BM763262	K-EST0044	C 795	18	1.1	764	8	AQ738662	AQ738662
C 723	18	1.1	729	7	CN294472	CN294472	170004241	C 796	18	1.1	764	9	CG020419	CG020419
C 724	18	1.1	730	4	CF766764	CF766764	603195631	C 797	18	1.1	765	6	CR092220	CR092220
C 725	18	1.1	730	7	BU465371	BU465371	603777709	C 798	18	1.1	765	9	AG566289	AG566289
C 726	18	1.1	731	5	BU491813	BU491813	604131727	C 799	18	1.1	767	7	CK246119	CK246119
C 727	18	1.1	732	5	BN755967	BN755967	ID0AA17B	C 800	18	1.1	767	7	CK865671	CK865671
C 728	18	1.1	732	7	BP152942	BP152942	BP152942	C 801	18	1.1	768	6	CA917697	CA917697
C 729	18	1.1	733	5	BU490541	BU490541	604131042	C 802	18	1.1	768	8	BZ639917	BZ639917
C 730	18	1.1	735	7	CF444619	CF444619	ES1680964	C 803	18	1.1	768	8	CG276764	CG276764
C 731	18	1.1	735	7	AG182762	AG182762	Pan t'rog1	C 804	18	1.1	769	5	BU416685	BU416685
C 732	18	1.1	735	7	CN053640	CN053640	Salamande	C 805	18	1.1	770	5	CK127178	CK127178
C 733	18	1.1	736	1	AA967722	AA967722	uh04a09..x	C 806	18	1.1	770	7	BF038815	BF038815
C 734	18	1.1	736	5	AX717524	AX717524	BX717524	C 807	18	1.1	771	2	CG691815	CG691815
C 735	18	1.1	736	9	AG444357	AG444357	Mus muscu	C 808	18	1.1	771	7	CC560438	CC560438
C 736	18	1.1	736	9	CG391711	CG391711	ZMMBBc057	C 809	18	1.1	772	7	CK127211	CK127211
C 737	18	1.1	736	9	AG182762	AG182762	Forward s	C 810	18	1.1	772	9	CG256745	CG256745
C 738	18	1.1	737	9	CN793801	CN793801	4128880 B	C 811	18	1.1	773	7	CR873191	CR873191
C 739	18	1.1	737	9	CL652689	CL652689	PR10115c	C 812	18	1.1	775	7	CR869731	CR869731
C 740	18	1.1	739	5	AX093469	AX093469	BX093469	C 813	18	1.1	776	7	CK142473	CK142473
C 741	18	1.1	739	9	CE151013	CE151013	ligr-gss-	C 814	18	1.1	776	7	CO101313	CO101313
C 742	18	1.1	740	8	AZ244786	AZ244786	RPCI-23-4	C 815	18	1.1	776	9	CG698678	CG698678
C 743	18	1.1	741	9	CK025140	CK025140	AGENCOURT	C 816	18	1.1	777	7	CR872867	CR872867
C 744	18	1.1	741	9	CL737593	CL737593	OR_BBA007	C 817	18	1.1	777	8	BH321589	BH321589
C 745	18	1.1	742	9	CR007615	CR007615	Forward s	C 818	18	1.1	778	7	CC611222	CC611222
C 746	18	1.1	743	5	BP433720	BP433720	BP433720	C 819	18	1.1	778	7	CG871227	CG871227
C 747	18	1.1	743	5	BU491238	BU491238	604130127	C 820	18	1.1	778	8	BZ546495	BZ546495
C 748	18	1.1	743	5	BU491311	BU491311	604131280	C 821	18	1.1	779	9	CC699800	CC699800
C 749	18	1.1	743	9	CG911055	CG911055	t064o20ba	C 822	18	1.1	779	9	CL236331	CL236331
C 750	18	1.1	744	5	AU141032	AU141032	AU141032	C 823	18	1.1	781	6	CH514418	CH514418
C 751	18	1.1	744	5	BO864656	BO864656	OGC27F10.	C 824	18	1.1	782	5	BU488564	BU488564
C 752	18	1.1	744	7	CK315763	CK315763	SB02026B2	C 825	18	1.1	783	5	BZ058247	BZ058247
C 753	18	1.1	744	7	CO160352	CO160352	FLD1_20.A	C 826	18	1.1	782	8	BP446124	BP446124
C 754	18	1.1	744	9	CG252795	CG252795	OGXDY23TH	C 827	18	1.1	783	9	CR137453	CR137453

[illegible]

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974 18 1.1 867 7 CN167671 AGENCOURT
975 18 1.1 867 8 BZ639922 OGCBOV05TM
976 18 1.1 868 2 BE539135 601061595
977 18 1.1 868 9 CG176984 PUF0A70TD
978 18 1.1 869 4 BG531389 602559640
979 18 1.1 870 7 CN326644 AGENCOURT
980 18 1.1 871 6 CA496252 AGENCOURT
981 18 1.1 872 4 BI858733 603386325
982 18 1.1 873 7 CN320420 AGENCOURT
983 18 1.1 873 7 CK872123 AGENCOURT
984 18 1.1 874 7 CL725714 OR_BA005
985 18 1.1 875 2 CN330403 AGENCOURT
986 18 1.1 875 2 BE570325 601333205
987 18 1.1 875 8 BZ283509 CH230-286
988 18 1.1 875 5 CG249875 OGW1S75TV
989 18 1.1 876 5 BU165923 603670985
990 18 1.1 876 7 CN329994 AGENCOURT
991 18 1.1 877 5 CG997475 ZUABP94TH
992 18 1.1 878 5 BX400411 BX400411
993 18 1.1 879 7 CN322875 AGENCOURT
994 18 1.1 879 8 BZ742467 OGFNC247C
995 18 1.1 879 9 CG335109 OGB2120TH
996 18 1.1 882 2 BF789402 602103450
997 18 1.1 882 2 CG847013 ND1_30C11
998 18 1.1 882 9 CG318903 OG1DM50TH
999 18 1.1 883 7 CN323208 AGENCOURT
1000 18 1.1 883 8 CC141792 ND1_51D20
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ALIGNMENTS

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RESULT 1
LOCUS AU237072 596 bp mRNA linear EST 01-APR-2002
DEFINITION AU237072 RAFIL5 Arabidopsis thaliana cDNA clone RAFIL5-47-A08 5',
            mRNA sequence.
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ACCESSION AU237072
VERSION AU237072.1 GI:19876241
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 596)

REFERENCE 1 (bases 1 to 596)

Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J.,

Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A.,

Muramatsu, M., Hayashizaki, Y., and Shinozaki, K.

Large scale analysis of Arabidopsis full-length cDNA

Unpublished (2002)

CONTACT: Motoaki Seki

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: msek@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source 1..596 Location/Qualifiers

/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-47-A08"
/cbase_type="mixture of silique and flower"

/lab_host="DH10B"
/clone_lib="RAFL15"
/note="Site_1: BamHI; Site_2: SalI"

ORIGIN

Query Match 25.0%; Score 410; DB 1; Length 596;
Best local Similarity 100.0%; Pred. No. 2,2e-221;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGAGGAGTAATGGAATCAGTAACGAGCTTCCTTCAACCGTCAATCGCCGTTTCTTCTG 60
DB 110 ATGGAGGAGTAATGGAATCAGTAACGAGCTTCCTTCAACCGTCAATCGCCGTTTCTTCTG 169
QY 61 ATTTGCGGTGCGCAACTCGCGTGGAGATGAGACCGAGTTTCAACGCGACTTCTGAG 120
DB 170 ATTTGCGGTGCGCAACTCGCGTGGAGATGAGACCGAGTTTCAACGCGACTTCTGAG 229
QY 121 CTATCGGGTATATCATTTCCGGGATTTCCGTCGACGACGATGAGCGGTGCTCATCTT 180
DB 230 CTATCGGGTATATCATTTCCGGGATTTCCGTCGACGACGATGAGCGGTGCTCATCTT 289
QY 181 GACTGTCCATCACTCCGTTGGAATCCGCTCGACCTCGATGCTAGACCACT 240
DB 290 GACTGTCCATCACTCCGTTGGAATCCGCTCGACCTCGATGCTAGACCACT 349
QY 241 AAGCTTCTTCTGCTGTCGACGCTGTTTAAAGTATGCTGATGATCTTTATATCA 300
DB 350 AAGCTTCTTCTGCTGTCGACGCTGTTTAAAGTATGCTGATGATCTTTATATCA 409
QY 301 ACAGACCATCCGAGTGAATGTCAGCGCTGACGAGTGTCTTTAGCATCAAGAAATG 360
DB 410 ACAGACCATCCGAGTGAATGTCAGCGCTGACGAGTGTCTTTAGCATCAAGAAATG 469
QY 361 GATCCAGTTTACATACAGGTCCTCTTTCTTCACTCTGGAAGAGTGCT 410
DB 470 GATCCAGTTTACATACAGGTCCTCTTTCTTCACTCTGGAAGAGTGCT 519
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RESULT 2
LOCUS BH944186 625 bp DNA linear GSS 01-OCT-2002
DEFINITION Obu90802.b1 B. oleracea002 Brassica oleracea genomic, genomic survey
            sequence.
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ACCESSION BH944186
VERSION BH944186.1 GI:23424246
KEYWORDS GSS.

SOURCE Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 625)

REFERENCE 1 (bases 1 to 625)

Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,

Nash, W., Rabinowitz, P.D. and Wilson, R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

CONTACT: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@wustl.wustl.edu

Plate: Obu90 row: a column: 02

Seq primer: -21upor forward

Class: shotgun

High quality sequence start: 45

High quality sequence stop: 398.

FEATURES

source 1..625 Location/Qualifiers

/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B. oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear

prep using *Brassica oleracea* T01000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN

Query Match 4.0%; Score 65; DB 8; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 586 ATGGGTAATATGCTTTCAGATCTTCTGGAATGCTGAGGCTGAGAAATGACCAAAA 645
Db 347 ATGGGTAATATGCTTTCAGATCTTCTGGAATGCTGAGGCTGAGAAATGACCAAAA 406

Qy 646 CATTA 650
Db 407 CATTA 411

RESULT 3
CC948085 546 bp DNA linear GSS 18-AUG-2003

LOCUS BOIHF12TR BO.1.4.1.6 KB nuc *Brassica oleracea* genomic clone
DEFINITION Whole genome survey sequence.

ACCESSION CC948085
VERSION CC948085.1 GI:33782462

KEYWORDS GSS.
SOURCE *Brassica oleracea*

ORGANISM *Brassica oleracea*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; *Brassica*.

REFERENCE 1 (bases 1 to 546)
Town,C.D., Van Aken,S., Utechtack,T., Koo,H. and Fraser,C.M.
AUTHORS Whole genome shotgun sequencing of *Brassica oleracea*
TITLE Unpublished (2001)
JOURNAL Other GSS: BOIHF12TR
COMMENT Contact: Chris Town

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208

Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source Location/Qualifiers

1..546
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOIHF12"
/clone_lib="BO.1.4.1.6 KB nuc"
/note="Vector: pHO52; Site 1: BcXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHO52 using BcXI linkers"

ORIGIN

Query Match 3.5%; Score 58; DB 9; Length 546;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 715 GTTAGGCAATCAATCTACTCTCTCTGCTGAACGTTGGCTTCCTGTTCTGAGG 772
Db 249 GTTAGGCAATCAATCTACTCTCTCTGCTGAACGTTGGCTTCCTGTTCTGAGG 306

RESULT 4
AJ589191 249 bp DNA linear GSS 15-JAN-2004
LOCUS AJ589191
DEFINITION *Arabidopsis thaliana* T-DNA flanking sequence, left border, clone
361B03, genomic survey sequence.

ACCESSION AJ589191
VERSION AJ589191.1 GI:37938815
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE *Arabidopsis thaliana* (thale cress)

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; *Arabidopsis*.

REFERENCE

1
Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruad,C., Denose,R., Pelletier,G.,
Lepointec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the *Arabidopsis* genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565

2 (bases 1 to 249)

REFERENCE Balzerque,S.
AUTHORS Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT

PCR was performed on DNA from transformants of *Arabidopsis thaliana*
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES

source

Location/Qualifiers
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/cultivar="Wassilewskija"
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="T-DNA flanking sequence
left border"

misc_feature

ORIGIN

Query Match 3.5%; Score 57; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.7e-20;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1336 AGGCTGGAAGTGGTTGATGGAGACGCTGACCTTAATCTGAGGATGAGACGCTA 1392
Db 190 AGGCTGGAAGTGGTTGATGGAGACGCTGACCTTAATCTGAGGATGAGACGCTA 134

RESULT 5

BZ082259 703 bp DNA linear GSS 10-OCT-2002
LOCUS BZ082259
DEFINITION IKV30d04.b1 B.oleracea002 *Brassica oleracea* genomic, genomic survey
sequence.

ACCESSION BZ082259
VERSION BZ082259.1 GI:23708975

KEYWORDS

GSS.
SOURCE *Brassica oleracea*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; *Brassica*.

REFERENCE

1 (bases 1 to 703)
Delehaunty,K., Powell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
AUTHORS Whole genome shotgun reads from *Brassica oleracea*
unpublished (2002)

COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: 1kv30 row: d column: 04
Seq primer: -21uppor forward
Class: shotgun
High quality sequence start: 77
High quality sequence stop: 551.
Location/Qualifiers

FEATURES
source
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/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN
Query Match 3.5%; Score 57; DB 8; Length 703;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1174 CTGACTCGTGGAGACACACCTATAAATGATTTGGCATATATGCTCAT 1230
|||||
92 CTGACTCTTGGAGACACCTATATAAATGATTTGGCATATATGCTCAT 148

DB

RESULT 6
LOCUS BH974466/c
DEFINITION BH974466 673 bp DNA linear GSS 02-OCT-2002
cdj06g04.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
Sequence.
ACCESSION BH974466
VERSION BH974466.1 GI:23457469
KEYWORDS GSS.
SOURCE
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 673)
Delehanthy,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: cdj06 row: g column: 04
Seq primer: -21uppor forward
Class: shotgun
High quality sequence start: 16
High quality sequence stop: 551.
Location/Qualifiers

FEATURES
source
1..673
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN
Query Match 2.9%; Score 47; DB 8; Length 673;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1249 TATTACTTTGCCCAAGTGGCAACCTTATCTGTATATTGATCAT 1235
|||||
570 TATTACTTTGCCCAAGTGGCAACCTTATCTGTATATTGATCAT 524

DB

RESULT 7
LOCUS BH864615/c
DEFINITION SALK_096352 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_096352, genomic survey sequence.
ACCESSION BH864615
VERSION BH864615.1 GI:22100513
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 40)
Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadgilab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednib,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of Atig04010.
Class: TDNA tagged.
Location/Qualifiers

FEATURES
source
1..40
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone_lib="SALK_096352"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN
Query Match 2.4%; Score 40; DB 8; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AATTGAAATCAGTAACGGCTTCTTCATCGCGG 49
|||||
40 AATTGAAATCAGTAACGGCTTCTTCATCGCGG 1

DB

RESULT 8
LOCUS BH847141/c
DEFINITION SALK_013495.53.90.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_013495.53.90.x, genomic
survey sequence.
ACCESSION BH847141

VERSION BH847141.1 GI:21418012
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 70)
 REFERENCE Alonzo, J.M., Lejse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shum, P., Zimmerman, J., and Ecker, J.R.
 A sequence-indexed library of insertion mutations in the
 Arabidopsis genome
 Unpublished (2001)
 JOURNAL Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: jecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At1g04010.
 Class: TDNA tagged.
 Location/Qualifiers
 1..70
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_013495.53.90.x"
 /clone.lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN

Query Match 2.0%; Score 33; DB 8; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1459 CAGCCAGAACGATGGAAGCAGCTACATG 1491
 |||||
 33 CAGCCAGAACGATGGAAGCAGCTACATG 1

DB

RESULT 9
 BH746163 207 bp DNA linear GSS 25-FEB-2002
 LOCUS q078e11.1 Bobuds01 Brassica oleracea genomic clone q078e11 5',
 DEFINITION genomic survey sequence.
 ACCESSION BH746163
 VERSION BH746163.1 GI:10881051
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosid II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 207)
 REFERENCE Karati, M., O'Shaughnessy, A., Palmer, L., Bahret, A., Baker, J.,
 Karati, V., Cummins, D.M., Katzenberger, F., King, L., Kirschhoff, K.,
 Kull, R., Miller, B., Muller, S., Nascimben, L., Preston, R.,
 Santos, L., Shah, R., Zutavern, T., Dedina, N., Rabinowicz, P.D. and
 McCombie, W.R.
 Whole Genome Shotgun Reads from Brassica oleracea (2002b)
 Unpublished (2002)
 JOURNAL Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: q078 row: e column: 11
 Seq primer: -21univfw
 Class: Shotgun
 High quality sequence stop: 207.
 Location/Qualifiers
 1..207
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /db_xref="taxon:3712"
 /clone="q078e11"
 /clone.lib="Bobuds01"
 /note="Vector: M13 for .x reads, pBluescript for .b and .g
 reads, Site_1: EcoRV; whole genome shotgun library from
 flowering buds. DNA was purified from a crude nuclear prep
 using Brassica oleracea TO1000DH3 buds provided by Thomas
 Osborn at the University of Wisconsin. Genomic DNA
 provided by Pablo Rabinowicz (CSHL) and shotgun library
 prepared in McCombie Lab."

ORIGIN

Query Match 2.0%; Score 32; DB 8; Length 207;
 Best Local Similarity 100.0%; Pred. No. 6.5e-06;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 586 ATGGGTAATATGCTTCAGATCTTCTGCA 617
 |||||
 118 ATGGGTAATATGCTTCAGATCTTCTGCA 149

DB

RESULT 10
 AU306500 728 bp mRNA linear EST 22-JAN-2004
 LOCUS AU306500 zinnia cultured mesophyll cell equalized cDNA zinnia
 DEFINITION elegans cDNA clone Z16086, mRNA sequence.
 ACCESSION AU306500
 VERSION AU306500.1 GI:41122436
 KEYWORDS EST.
 SOURCE Zinnia elegans
 ORGANISM Zinnia elegans
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Zinnia.
 1 (bases 1 to 728)
 REFERENCE Demura, T., Tashiro, G., Horiguchi, G., Kishimoto, N., Kubo, M.,
 Matsuno, N., Minami, A., Nagata-Hiwatashi, M., Nakamura, K.,
 Okamura, Y., Sassa, N., Suzuki, S., Yasaki, J., Kikuchi, S. and
 Fukuda, H.
 Visualization by comprehensive microarray analysis of gene
 expression programs during transdifferentiation of mesophyll cells
 into xylem cells
 Proc. Natl. Acad. Sci. U.S.A. 99 (24), 15794-15799 (2002)
 JOURNAL Contact: Taku Demura
 Morphogenesis Research Group
 RIKEN Plant Science Center
 1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9605
 Fax: 81-45-503-9573
 Email: demura@postman.riken.go.jp
 This clone was obtained at our laboratory
 Seq primer: M13 forward.
 Location/Qualifiers
 1..728
 /organism="Zinnia elegans"
 /mol_type="mRNA"
 /cultivar="Canary bird"
 /db_xref="taxon:34245"
 /clone="Z16086"
 /tissue_type="mesophyll cell"

/clone_11b="zinnia cultured mesophyll cell equalized cDNA"
/note="Vector: pGEM-T easy; cultured in triacetyl medium"

ORIGIN

Query Match 1.8%; Score 30; DB 1; Length 728;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 688 GCTGTTGAGCTCCTCTTCTGTTCTGTT 717
|||||
249 GCTGTTGAGCTCCTCTTCTGTTCTGTT 278
|||||

RESULT 11
LOCUS BH548609 303 bp DNA linear GSS 14-DEC-2001
DEFINITION BOHCO62TR BOHC Brassica oleracea genomic clone BOHCO62, genomic survey sequence.
ACCESSION BH548609
VERSION BH548609.1 GI:17800389
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 303)
Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea unpublished (2001)
JOURNAL Other_GSSs: BOHCO62TR
AUTHORS Other_GSSs: BOHCO62TR
TITLE Contact: Chris Town
JOURNAL TIGR
COMMENT 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TP
Class: sheared ends.
Location/Qualifiers
1..303
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHCO62"
/clone_11b="BOHC"
/note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 1.8%; Score 29; DB 8; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 GAGTGCTTAAGTGTGTGAGTTGG 431
|||||
212 GAGTGCTTAAGTGTGTGAGTTGG 184
|||||

RESULT 12
LOCUS B11175 1225 bp DNA linear GSS 14-MAY-1997
DEFINITION F14L4-Sp6 IGF Arabidopsis thaliana genomic clone F14L4, genomic survey sequence.
ACCESSION B11175
VERSION B11175.1 GI:2092305
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1225)
Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and Ecker,J.
JOURNAL BAC End Sequences at ATGC
COMMENT Unpublished (1997)
Other_GSSs: F14L4-T7
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA 19104
Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
Seq primer: Sp6
Class: BAC ends
High quality sequence start: 155
High quality sequence stop: 221.
Location/Qualifiers
1..1225
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="F14L4"
/sex="hermaphrodite"
/clone_11b="IGF"
/note="Vector: BelobacII; Site_1: EcoRI; Site_2: EcoRI; Produced by Thomas Altmann"

ORIGIN

Query Match 1.7%; Score 28; DB 8; Length 1225;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 AGCGTGTCGATCCTTGACTGCATAC 192
|||||
209 AGCGTGTCGATCCTTGACTGCATAC 236
|||||

RESULT 13
LOCUS B1922233 632 bp mRNA linear EST 17-OCT-2001
DEFINITION EST542136 tomato callus Lycopersicon esculentum cDNA clone CUEC76P18 5' end, mRNA sequence.
ACCESSION B1922233
VERSION B1922233.1 GI:16218653
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 632)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Uteback,T., Van Aken,S., Romling,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato callus tissue (2001)
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics Institute
Seq primer: T3.
Location/Qualifiers
1..632
/organism="Lycopersicon esculentum"
/mol_type="mRNA"

/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC76P18"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato callus"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST library"

ORIGIN

Query Match 1.5%; Score 24; DB 4; Length 632;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 688 GCTGTGGAGCTCCTCTTGTGT 711
Db 540 GCTGTGGAGCTCCTCTTGTGT 563

RESULT 14
BI422757 704 bp mRNA linear EST 16-AUG-2001
LOCUS B1422757
DEFINITION EST533423 tomato callus, TAMU Lycopersicon esculentum cDNA clone
VERSION B1422757
KEYWORDS EST.
SOURCE B1422757.1 GI:15197439
ORGANISM Lycopersicon esculentum (tomato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 704)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, L.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Romling, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.

REFERENCE

AUTHORS

TITLE
JOURNAL
COMMENT
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES

SOURCE

1..704
location/Qualifiers
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC71P15"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato callus, TAMU"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST library"

ORIGIN

Query Match 1.5%; Score 24; DB 4; Length 704;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 688 GCTGTGGAGCTCCTCTTGTGT 711
Db 540 GCTGTGGAGCTCCTCTTGTGT 563

RESULT 15
CK259393 788 bp mRNA linear EST 03-AUG-2004
LOCUS CK259393
DEFINITION EST705471 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAB029 5' end, mRNA sequence.
VERSION CK259393
KEYWORDS CK259393.1 GI:39816371
EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Other ESTs: EST705470 EST705472 EST705473
Contact: Robin Buehl
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ATG TAG GTG ACA CTA TAG.

FEATURES

SOURCE

1..788
location/Qualifiers
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAB029"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Query Match 1.5%; Score 24; DB 7; Length 788;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 688 GCTGTGGAGCTCCTCTTGTGT 711
Db 11 GCTGTGGAGCTCCTCTTGTGT 34

Search completed: November 9, 2004, 10:07:44
Job time : 5505 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: November 9, 2004, 02:27:12 ; Search time 7038 Seconds
(without alignment)
11026.200 Million cell updates/sec

Title: US-09-651-651-4
Perfect score: 1641
Sequence: 1 atggagagcgaattcgaatc.....ctgataaagtgggtactaa 1641

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:.*
1: gb_ba:.*
2: gb_hcg:.*
3: gb_in:.*
4: gb_om:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_ars:.*
12: gb_ey:.*
13: gb_un:.*
14: gb_vl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1641	100.0	1641	6	AX090311 Sequence
2	243	14.8	3896	2	BD271623 Novel cla
3	243	14.8	3896	6	BD271623 Novel cla
4	243	14.8	3896	6	AX037587 Sequence
5	243	14.8	3896	6	AX037606 Sequence
6	243	14.8	119914	8	AC003027 Arabidops
7	27	1.6	44	6	AX090361 Sequence
8	26	1.6	40	6	AX090362 Sequence
9	25	1.5	2609	8	AP493159 Medicine
10	21	1.3	2638	3	TRBVSGAAB
11	21	1.3	38785	9	AC073933 Homo sapi
12	21	1.3	70206	5	AL929207 Zebrafish
13	21	1.3	74349	9	AL603869 Human DNA
14	21	1.3	93398	8	AP006356 Lotus cor
15	21	1.3	107430	9	AC006988 Homo sapi
16	21	1.3	110000	2	BX813304 Dario rer
17	21	1.3	119797	2	AC013236 Drosophila
18	21	1.3	128623	3	AC092245 Drosophila
19	21	1.3	134866	10	AL8444206 Mouse DNA

C	20	1.3	150797	2	CR352294	CR352294 Dario rer
C	21	1.3	174974	3	AC092228	AC092228 Drosophila
C	22	1.3	186945	2	AC11427	AC11427 Rattus no
C	23	1.3	192586	10	AL645972	AL645972 Mouse DNA
C	24	1.3	210702	5	BX119982	BX119982 Zebrafish
C	25	1.3	215899	5	BX004818	BX004818 Zebrafish
C	26	1.3	223940	2	AC087567	AC087567 Mus muscu
C	27	1.3	228999	2	AC083885	AC083885 Homo sapi
C	28	1.3	263309	3	AE003644	AE003644 Drosophila
C	29	1.3	300962	3	DROSADH04	DROSADH04 Drosophila
C	30	1.2	427	11	G61455	G61455 SHC-85644
C	31	1.2	595	11	BV067360	BV067360 S209P6185
C	32	1.2	1667	14	HH006940	HH006940 Human hepe
C	33	1.2	7768	1	AF041837	AF041837 Buchnera
C	34	1.2	10242	1	AE000827	AE000827 Methanoba
C	35	1.2	25403	3	U64609	U64609 Caenorhabdi
C	36	1.2	63902	1	AY258503	AY258503 Escherich
C	37	1.2	75145	9	HS362G17	HS362G17 Human DNA
C	38	1.2	80182	5	AL772356	AL772356 Zebrafish
C	39	1.2	85905	2	AC133571	AC133571 Medicago
C	40	1.2	92799	2	AC135817	AC135817 Rattus no
C	41	1.2	93533	5	AL672129	AL672129 Zebrafish
C	42	1.2	96694	9	AC090470	AC090470 Homo sapi
C	43	1.2	110000	2	AP006500_09	AP006500_09 Conlunction (10 o
C	44	1.2	110695	9	AC010306	AC010306 Homo sapi
C	45	1.2	110758	8	AC147774	AC147774 Medicago
C	46	1.2	112027	9	AC073502	AC073502 Homo sapi
C	47	1.2	115626	9	AC103792	AC103792 Homo sapi
C	48	1.2	122897	2	AP001953	AP001953 Homo sapi
C	49	1.2	136228	2	AC067916	AC067916 Homo sapi
C	50	1.2	140547	2	AC147821	AC147821 Mus muscu
C	51	1.2	145248	5	AL935292	AL935292 Zebrafish
C	52	1.2	146245	2	AC148388	AC148388 Rhinophlo
C	53	1.2	147544	2	AC135325	AC135325 Homo sapi
C	54	1.2	14845	2	HS114A1	HS114A1 Human DNA
C	55	1.2	149879	2	AP005381	AP005381 Oryza sat
C	56	1.2	157093	2	AC006916	AC006916 Caenorhab
C	57	1.2	157797	8	AP005184	AP005184 Oryza sat
C	58	1.2	158792	8	AP003833	AP003833 Oryza sat
C	59	1.2	160869	2	AC147815	AC147815 Xenopus t
C	60	1.2	163183	9	AC016574	AC016574 Homo sapi
C	61	1.2	166651	4	AC087160	AC087160 Sus scrof
C	62	1.2	167137	2	AC150859	AC150859 Bos tauru
C	63	1.2	169588	8	AP006461	AP006461 Oryza sat
C	64	1.2	170777	2	AC148444	AC148444 Rhinophlo
C	65	1.2	171375	2	CNS01DSK	CNS01DSK Human chr
C	66	1.2	171817	2	BX928757	BX928757 Dario rer
C	67	1.2	171940	2	AC148514	AC148514 Papio anu
C	68	1.2	174147	2	AC148048	AC148048 Ootlemur
C	69	1.2	175326	9	CNS01DIO	CNS01DIO Human chr
C	70	1.2	175326	2	CR678095	CR678095 Dario rer
C	71	1.2	176259	2	AC101748	AC101748 Mus muscu
C	72	1.2	178157	2	AC101809	AC101809 Mus muscu
C	73	1.2	183298	2	BX571737	BX571737 Dario rer
C	74	1.2	184266	2	AC148555	AC148555 Callithr
C	75	1.2	185397	2	BX640499	BX640499 Dario rer
C	76	1.2	185967	9	AC015721	AC015721 Homo sapi
C	77	1.2	188333	9	AC116588	AC116588 Mus muscu
C	78	1.2	189927	2	AC148944	AC148944 Gaeterost
C	79	1.2	192452	2	AC027105	AC027105 Homo sapi
C	80	1.2	194974	2	AC139362	AC139362 Homo sapi
C	81	1.2	195033	9	AC087463	AC087463 Homo sapi
C	82	1.2	196918	9	AC002461	AC002461 Homo sapi
C	83	1.2	197273	2	AC026092	AC026092 Homo sapi
C	84	1.2	197351	2	AC139241	AC139241 Mus muscu
C	85	1.2	200361	10	BX324158	BX324158 Dario rer
C	86	1.2	200875	2	AL6633052	AL6633052 Mouse DNA
C	87	1.2	202972	10	AC146059	AC146059 Pan trogl
C	88	1.2	210466	2	AC094246	AC094246 Rattus no
C	89	1.2	232923	5	AL935307	AL935307 Zebrafish
C	90	1.2	234744	2	AC093340	AC093340 Mus muscu
C	91	1.2	234826	2	AC094325	AC094325 Rattus no
C	92	1.2	234909	2	AC094325	AC094325 Rattus no

C 93	20	1.2	240901	2	AC096328	C 166	19	1.2	100000	9	AP000520	AP000520 Homo sapi
C 94	20	1.2	246877	2	AC137365	C 167	19	1.2	101281	2	AC026389	AC026389 Homo sapi
C 95	20	1.2	250510	2	AC098055	C 168	19	1.2	104017	2	AC105050	AC105050 Homo sapi
C 96	20	1.2	255349	2	AC095800	C 169	19	1.2	105633	9	AL671561	AL671561 Human DNA
C 97	20	1.2	256219	2	AC095416	C 170	19	1.2	107164	9	AL449105	AL449105 Human DNA
C 98	20	1.2	256320	2	AC109981	C 171	19	1.2	110000	1	AE017225_45	Continuation (46 o
C 99	20	1.2	265723	2	AC106686	C 172	19	1.2	110000	1	AE017324_45	Continuation (46 o
C 100	20	1.2	273684	2	AC113630	C 173	19	1.2	110000	1	AE017354_45	Continuation (46 o
C 101	20	1.2	273684	2	AC108628	C 174	19	1.2	110000	1	AP003358_2	Continuation (3 of
C 102	19	1.2	294461	2	AC108628	C 175	19	1.2	110000	1	BX571856_02	Continuation (3 of
C 103	19	1.2	442	10	MUSAH05	C 176	19	1.2	110000	2	AC091446_2	Continuation (3 of
C 104	19	1.2	571	11	BV036511	C 177	19	1.2	110000	2	AC105793_4	Continuation (5 of
C 105	19	1.2	675	6	CO714589	C 178	19	1.2	110000	2	CEY10588_4	Continuation (5 of
C 106	19	1.2	677	10	RATCPA4	C 179	19	1.2	110000	2	LMFLCHR26_0	Continuation (5 of
C 107	19	1.2	1310	10	RNCPPA	C 180	19	1.2	110000	2	AC004741	Continuation (5 of
C 108	19	1.2	1337	4	BTCARPEP	C 181	19	1.2	112242	9	AC004741	Continuation (5 of
C 109	19	1.2	1362	4	BOVCARBP	C 182	19	1.2	114707	2	AC146332	Continuation (3 of
C 110	19	1.2	1607	10	RATCBXPA	C 183	19	1.2	118192	8	AP004120	Continuation (3 of
C 111	19	1.2	1775	10	BC055778	C 184	19	1.2	121341	10	BX005469	Continuation (3 of
C 112	19	1.2	1785	8	HOTUBB2	C 185	19	1.2	123078	8	AP004902	Continuation (3 of
C 113	19	1.2	2372	6	CO796156	C 186	19	1.2	125405	8	BX927141	Continuation (3 of
C 114	19	1.2	2372	6	CO796157	C 187	19	1.2	128757	2	AC142568	Continuation (3 of
C 115	19	1.2	2372	6	CO796158	C 188	19	1.2	129516	8	ATP24M12	Continuation (3 of
C 116	19	1.2	2372	6	CO796159	C 189	19	1.2	129611	9	AL645935	Continuation (3 of
C 117	19	1.2	2372	6	CO796160	C 190	19	1.2	130558	2	AC148793	Continuation (3 of
C 118	19	1.2	2372	6	CO796161	C 191	19	1.2	131368	9	CR388220	Continuation (3 of
C 119	19	1.2	2372	6	CO796162	C 192	19	1.2	131860	2	AC102708	Continuation (3 of
C 120	19	1.2	2372	6	CO796163	C 193	19	1.2	132775	8	AC046156	Continuation (3 of
C 121	19	1.2	2372	6	CO796164	C 194	19	1.2	132875	8	AC135461	Continuation (3 of
C 122	19	1.2	2372	6	CO796165	C 195	19	1.2	133176	2	AC138445	Continuation (3 of
C 123	19	1.2	2372	6	CO796166	C 196	19	1.2	134019	3	AC006471	Continuation (3 of
C 124	19	1.2	2372	6	CO796167	C 197	19	1.2	137072	2	AL353893	Continuation (3 of
C 125	19	1.2	2372	6	CO796168	C 198	19	1.2	137924	2	AL353893	Continuation (3 of
C 126	19	1.2	2372	6	CO796169	C 199	19	1.2	139215	8	AC126780	Continuation (3 of
C 127	19	1.2	2372	6	CO796170	C 200	19	1.2	139793	9	AC125629	Continuation (3 of
C 128	19	1.2	2372	6	CO796171	C 201	19	1.2	140739	9	AP005432	Continuation (3 of
C 129	19	1.2	2372	6	CO796172	C 202	19	1.2	142152	2	AC139658	Continuation (3 of
C 130	19	1.2	2372	6	CO796173	C 203	19	1.2	143461	2	AC141021	Continuation (3 of
C 131	19	1.2	2372	6	CO796174	C 204	19	1.2	144759	2	HS352A20	Continuation (3 of
C 132	19	1.2	2372	6	CO796175	C 205	19	1.2	147458	2	AC069591	Continuation (3 of
C 133	19	1.2	2488	6	CO796176	C 206	19	1.2	149094	5	AL929543	Continuation (3 of
C 134	19	1.2	2522	10	AR353989	C 207	19	1.2	147094	5	AL929543	Continuation (3 of
C 135	19	1.2	3111	8	BC033430	C 208	19	1.2	147123	8	AP005691	Continuation (3 of
C 136	19	1.2	3642	3	AK073117	C 209	19	1.2	147974	2	AC076970	Continuation (3 of
C 137	19	1.2	4123	3	AT344240	C 210	19	1.2	148438	2	AC019072	Continuation (3 of
C 138	19	1.2	4745	9	H0M0H1TRAN	C 211	19	1.2	149132	8	AC116949	Continuation (3 of
C 139	19	1.2	6010	9	HS0803666	C 212	19	1.2	150407	2	AC093228	Continuation (3 of
C 140	19	1.2	6142	8	HS0804621	C 213	19	1.2	151944	2	AC137701	Continuation (3 of
C 141	19	1.2	6142	8	CMRDNA1	C 214	19	1.2	152877	2	AC107399	Continuation (3 of
C 142	19	1.2	6581	9	CU0RGIS	C 215	19	1.2	154434	5	BX649404	Continuation (3 of
C 143	19	1.2	8500	9	H0M0HANTLE	C 216	19	1.2	154733	2	AC127462	Continuation (3 of
C 144	19	1.2	8552	1	HS4292348	C 217	19	1.2	154895	2	AC020329	Continuation (3 of
C 145	19	1.2	17500	2	AC017179	C 218	19	1.2	156328	2	AC148280	Continuation (3 of
C 146	19	1.2	29774	1	AF193754	C 219	19	1.2	157048	2	AC148303	Continuation (3 of
C 147	19	1.2	39108	9	BX284659	C 220	19	1.2	157207	9	BX640542	Continuation (3 of
C 148	19	1.2	41203	9	AC004194	C 221	19	1.2	158971	2	CR339053	Continuation (3 of
C 149	19	1.2	54631	1	AC074318	C 222	19	1.2	159427	2	AP004882	Continuation (3 of
C 150	19	1.2	58431	1	AC025591	C 223	19	1.2	160333	9	AL845454	Continuation (3 of
C 151	19	1.2	62282	9	AC010304	C 224	19	1.2	161406	9	AC145042	Continuation (3 of
C 152	19	1.2	62350	9	AC067725	C 225	19	1.2	162556	9	AP002376	Continuation (3 of
C 153	19	1.2	66893	2	AC105793_5	C 226	19	1.2	163025	14	AY372243	Continuation (3 of
C 154	19	1.2	70206	8	AC126804_3	C 227	19	1.2	163167	9	AC011347	Continuation (3 of
C 155	19	1.2	74298	8	AB020745	C 228	19	1.2	163538	9	AC012598	Continuation (3 of
C 156	19	1.2	76880	2	AC150175	C 229	19	1.2	163805	9	AC010956	Continuation (3 of
C 157	19	1.2	81561	9	AB023057	C 230	19	1.2	164612	10	AC142697	Continuation (3 of
C 158	19	1.2	87397	9	AL356778	C 231	19	1.2	166472	2	AC145009	Continuation (3 of
C 159	19	1.2	88619	9	AC097723	C 232	19	1.2	167214	2	AC096202	Continuation (3 of
C 160	19	1.2	88746	9	AC009321	C 233	19	1.2	168997	2	AC021927	Continuation (3 of
C 161	19	1.2	90872	2	AC006940	C 234	19	1.2	170167	10	AL672143	Continuation (3 of
C 162	19	1.2	92586	2	AC005978	C 235	19	1.2	170970	2	AC021564	Continuation (3 of
C 163	19	1.2	94212	2	AC150246	C 236	19	1.2	171158	2	AC122983	Continuation (3 of
C 164	19	1.2	95169	8	AP006084	C 237	19	1.2	172157	2	AC125832	Continuation (3 of
C 165	19	1.2	95379	9	AC106749	C 238	19	1.2	172613	10	AL591953	Continuation (3 of

C 239	19	1.2 172637	6	AX686783	Sequence	C 312	19	1.2 227595	2	CR450685	CR450685
C 240	19	1.2 174656	2	AC019249	Hom sapi	C 313	19	1.2 228187	2	AC127107	Rattus no
C 241	19	1.2 174710	2	AC069134	Hom sapi	C 314	19	1.2 228202	5	BX284664	Zebrafish
C 242	19	1.2 176362	2	AC149459	Papio anu	C 315	19	1.2 228540	2	AC132055	Rattus no
C 243	19	1.2 176544	2	AC138877	Hom sapi	C 316	19	1.2 230385	2	AC103227	Rattus no
C 244	19	1.2 176594	2	AC119325	Rattus no	C 317	19	1.2 230611	2	AC126655	Rattus no
C 245	19	1.2 177251	10	AC124565	Mus muscu	C 318	19	1.2 231172	2	AC116887	Rattus no
C 246	19	1.2 178730	2	AC148680	Macaca mu	C 319	19	1.2 233367	10	AC118931	Mus muscu
C 247	19	1.2 179712	2	AC135704	Rattus no	C 320	19	1.2 234817	10	AL663048	Mouse DNA
C 248	19	1.2 180133	2	AC113885	Rattus no	C 321	19	1.2 235024	2	AC120681	Rattus no
C 249	19	1.2 180816	2	AC110395	Rattus no	C 322	19	1.2 235545	2	AC103084	Rattus no
C 250	19	1.2 180976	3	AL513321	Gallus ga	C 323	19	1.2 235668	2	AC110729	Mus muscu
C 251	19	1.2 181955	3	AC008304	Human DNA	C 324	19	1.2 235681	2	AC150045	Gallus ga
C 252	19	1.2 183031	10	AL669952	Mouse DNA	C 325	19	1.2 235700	2	AC103577	Rattus no
C 253	19	1.2 183213	10	AL669952	Mouse DNA	C 326	19	1.2 235777	2	AC130900	Rattus no
C 254	19	1.2 183338	2	AC083775	Hom sapi	C 327	19	1.2 235814	2	AC106156	Rattus no
C 255	19	1.2 184021	2	AC093048	Drosophi	C 328	19	1.2 237787	2	AC098758	Rattus no
C 256	19	1.2 184231	3	AC023651	Hom sapi	C 329	19	1.2 237961	6	AX504841	Sequence
C 257	19	1.2 185147	2	AC147193	Papio anu	C 330	19	1.2 238365	2	AC107269	Rattus no
C 258	19	1.2 185560	2	AC129046	Rattus no	C 331	19	1.2 238452	2	AC097019	Rattus no
C 259	19	1.2 186301	5	AL356962	Human DNA	C 332	19	1.2 240181	2	AC098105	Rattus no
C 260	19	1.2 186380	5	BX004774	Zebrafish	C 333	19	1.2 241204	2	AC099185	Rattus no
C 261	19	1.2 186437	9	AC146079	Pan trogl	C 334	19	1.2 241420	2	AC094501	Rattus no
C 262	19	1.2 187088	10	AC133876	Mus muscu	C 335	19	1.2 241632	2	AC131461	Rattus no
C 263	19	1.2 187718	2	AC112084	Rattus no	C 336	19	1.2 243073	2	AC108537	Rattus no
C 264	19	1.2 188867	10	AC132012	Mus muscu	C 337	19	1.2 243056	2	AC127765	Rattus no
C 265	19	1.2 188914	9	AC093744	Hom sapi	C 338	19	1.2 248390	2	AC118791	Rattus no
C 266	19	1.2 189655	9	AC148670	Macaca mu	C 339	19	1.2 248682	2	AC103093	Rattus no
C 267	19	1.2 189767	9	AL137145	Human DNA	C 340	19	1.2 249900	2	AC097241	Rattus no
C 268	19	1.2 189840	9	AC012320	Hom sapi	C 341	19	1.2 250715	2	AC125673	Rattus no
C 269	19	1.2 190182	2	AC149861	Papio anu	C 342	19	1.2 253693	2	AC093997	Rattus no
C 270	19	1.2 191190	2	CR478286	Danio rer	C 343	19	1.2 256671	2	AC119533	Rattus no
C 271	19	1.2 191300	2	AC109020	Rattus no	C 344	19	1.2 257572	2	AC125574	Rattus no
C 272	19	1.2 191747	2	AC113675	Rattus no	C 345	19	1.2 262745	2	AE003658	Drosophi
C 273	19	1.2 193639	2	AC127619	Rattus no	C 346	19	1.2 262917	2	AC097239	Rattus no
C 274	19	1.2 194237	9	AC009063	Hom sapi	C 347	19	1.2 263069	2	AC103440	Rattus no
C 275	19	1.2 194362	10	AC124716	Mus muscu	C 348	19	1.2 263319	2	AC125258	Mus muscu
C 276	19	1.2 195031	10	AL845265	Mouse DNA	C 349	19	1.2 264095	9	AC008500	Hom sapi
C 277	19	1.2 195057	2	BX897664	Danio rer	C 350	19	1.2 264232	2	CR626890	Danio rer
C 278	19	1.2 195393	2	AC102703	Mus muscu	C 351	19	1.2 264904	2	AC121259	Mus muscu
C 279	19	1.2 196731	2	CR384092	Danio rer	C 352	19	1.2 267068	2	AC103090	Rattus no
C 280	19	1.2 196788	2	AC021626	Hom sapi	C 353	19	1.2 270098	2	AC097879	Rattus no
C 281	19	1.2 197170	2	AC133870	Mus muscu	C 354	19	1.2 272459	2	AC109059	Rattus no
C 282	19	1.2 198400	2	AC138091	Mus muscu	C 355	19	1.2 275060	2	AC135406	Rattus no
C 283	19	1.2 198638	2	AC139130	Mus muscu	C 356	19	1.2 276851	3	AC137860	Mus muscu
C 284	19	1.2 198794	2	AL583825	Human DNA	C 357	19	1.2 277607	2	CEY10588A	Caenorhab
C 285	19	1.2 198872	9	AF297093	Hom sapi	C 358	19	1.2 278375	2	AC130093	Rattus no
C 286	19	1.2 199819	2	AC148682	Macaca mu	C 359	19	1.2 279288	2	AC098526	Rattus no
C 287	19	1.2 201329	2	CR450778	Danio rer	C 360	19	1.2 287955	2	AC095777	Rattus no
C 288	19	1.2 201620	10	AC131746	Mus muscu	C 361	19	1.2 288794	1	AE017279	Bacillus
C 289	19	1.2 201862	2	AC150069	Gallus ga	C 362	19	1.2 291804	1	AE017039	Bacillus
C 290	19	1.2 202237	10	AC114825	Mus muscu	C 363	19	1.2 293933	2	AC090040	Hom sapi
C 291	19	1.2 202515	9	AC148690	Macaca mu	C 364	19	1.2 296050	1	AP003129	Staphyloc
C 292	19	1.2 203700	2	AC141410	Rattus no	C 365	19	1.2 299331	3	AE003460	Drosophi
C 293	19	1.2 204946	2	AC116145	Mus muscu	C 366	19	1.2 300235	2	AC123334	Rattus no
C 294	19	1.2 205178	2	AC132020	Rattus no	C 367	19	1.2 300893	1	AE017006	Bacillus
C 295	19	1.2 206538	2	AC111027	Mus muscu	C 368	19	1.2 300902	2	AC115580	Rattus no
C 296	19	1.2 209337	2	AC122682	Rattus no	C 369	19	1.2 300975	1	AE017013	Bacillus
C 297	19	1.2 209581	2	AC148275	Papio anu	C 370	19	1.2 301903	1	AE016969	Mycoplasma
C 298	19	1.2 209772	9	AC099782	Hom sapi	C 371	19	1.2 303992	2	AC118360	Rattus no
C 299	19	1.2 210616	2	BX324151	Danio rer	C 372	19	1.2 303996	2	AC092975	Hom sapi
C 300	19	1.2 211612	2	AC119144	Rattus no	C 373	19	1.2 312227	2	AC120960	Rattus no
C 301	19	1.2 212475	2	AC093021	Rattus no	C 374	19	1.2 314415	9	AC106697	Rattus no
C 302	19	1.2 214121	2	AC141575	Rattus no	C 375	19	1.2 314866	9	AF055066	Hom sapi
C 303	19	1.2 216080	2	AC150049	Gallus ga	C 376	19	1.2 315486	2	AC068887	Hom sapi
C 304	19	1.2 216330	2	AC098443	Rattus no	C 377	19	1.2 322058	2	HSU32611	Human pre-B
C 305	19	1.2 217711	10	AC116385	Mus muscu	C 378	19	1.1 125	6	AX900512	Sequence
C 306	19	1.2 218267	9	AC148667	Macaca mu	C 379	19	1.1 125	6	BD036045	Sequence
C 307	19	1.2 219553	2	HSN312687	Hom sapi	C 380	19	1.1 153	6	AX907220	Sequence
C 308	19	1.2 223717	2	AC108896	Bos tauru	C 381	19	1.1 153	6	BD042753	Sequence
C 309	19	1.2 223827	2	AC079441	Mus muscu	C 382	19	1.1 167	9	AY488883S19	Sequence
C 310	19	1.2 224219	2	AC115152	Rattus no	C 383	19	1.1 167	9	AY488929	Gorilla g
C 311	19	1.2 224936	2	AC106537	Rattus no	C 384	19	1.1 167	9	AY488937	Pongo pyg

C 385	18	1.1	167	9	AY488967519	C 458	18	1.1	2475	8	AK068162	AK068162	Oryza sat
386	18	1.1	241	6	AR280863	459	18	1.1	2629	6	AX078700	AX078700	Sequence
387	18	1.1	241	6	AR283359	C 460	18	1.1	2539	10	AF136751	AF136751	Mus muscu
388	18	1.1	241	6	AR344127	C 461	18	1.1	2673	8	AB032074	AB032074	Nicotiana
389	18	1.1	241	6	AR351328	C 462	18	1.1	2701	6	E26903	E26903	Novel potas
390	18	1.1	241	6	AR453908	C 463	18	1.1	2827	8	AK103089	AK103089	Oryza sat
391	18	1.1	241	6	AX030351	C 464	18	1.1	2827	8	AK110496	AK110496	Oryza sat
C 392	18	1.1	273	11	G73222	C 465	18	1.1	2855	10	AF337809	AF337809	Rattus no
393	18	1.1	300	6	BD219818	C 466	18	1.1	3078	8	KL040151	KL040151	Kluyveromyc
394	18	1.1	334	8	FV8508252	467	18	1.1	3149	6	CQ834736	CQ834736	Sequence
C 395	18	1.1	411	6	AX071678	468	18	1.1	3149	6	CQ834738	CQ834738	Sequence
C 396	18	1.1	444	5	AF369084	469	18	1.1	3190	9	AB056846	AB056846	Macaca fa
397	18	1.1	451	6	BD275888	470	18	1.1	3190	9	AB056847	AB056847	Macaca fa
398	18	1.1	451	6	AR220673	471	18	1.1	3268	6	HSGP1P137	HSGP1P137	Sequence
399	18	1.1	451	6	AR255667	C 472	18	1.1	3278	6	I32736	I32736	Sequence
400	18	1.1	451	6	AR281237	C 473	18	1.1	3278	6	HSM805773	HSM805773	Sequence
401	18	1.1	451	6	AX365932	C 474	18	1.1	3352	9	AB056621	AB056621	Acet clrc
402	18	1.1	458	6	AX156218	C 475	18	1.1	3380	8	AY566621	AY566621	Acet clrc
403	18	1.1	484	5	AP376130	476	18	1.1	3477	9	BC001731	BC001731	Homo sapi
404	18	1.1	489	6	AX311626	477	18	1.1	3521	6	BD235119	BD235119	Homo sapi
405	18	1.1	489	6	BD047159	478	18	1.1	3521	6	E31260	E31260	Human MP5
C 406	18	1.1	516	6	AX395894	479	18	1.1	3522	6	AB019005	AB019005	Homo sapi
C 407	18	1.1	525	6	CQ672104	480	18	1.1	3582	6	AX751713	AX751713	Sequence
C 408	18	1.1	550	4	AB060696	481	18	1.1	3760	9	BC034607	BC034607	Homo sapi
C 409	18	1.1	575	3	AP526256	C 482	18	1.1	3859	2	AC015166	AC015166	Drosophila
410	18	1.1	578	6	CQ522113	C 483	18	1.1	3887	6	AX876625	AX876625	Sequence
411	18	1.1	600	6	HSW30CF	C 484	18	1.1	3887	6	BD156228	BD156228	Primer fo
412	18	1.1	607	11	G19996	C 485	18	1.1	3887	6	AK001379	AK001379	Homo sapi
413	18	1.1	627	11	BV031831	486	18	1.1	4060	10	BC011271	BC011271	Mus muscu
414	18	1.1	631	8	AP320290	487	18	1.1	4385	6	AX753250	AX753250	Sequence
C 415	18	1.1	634	11	BY068201	C 488	18	1.1	4470	9	HSA223948	HSA223948	Homo sapi
C 416	18	1.1	648	11	G77415	489	18	1.1	4586	6	AR339039	AR339039	Sequence
C 417	18	1.1	779	3	AY617223	490	18	1.1	4662	3	CEY102ASB	CEY102ASB	Caenorhab
C 418	18	1.1	792	6	AX412851	491	18	1.1	4684	10	AB029482	AB029482	Mus muscu
419	18	1.1	792	6	AX505650	C 492	18	1.1	4931	5	CG716621	CG716621	Xenopus l
420	18	1.1	792	6	AX652052	C 493	18	1.1	5143	5	BC072296	BC072296	Sequence
421	18	1.1	792	8	AY097422	C 494	18	1.1	5329	3	DMU080FP	DMU080FP	Sequence
422	18	1.1	895	8	AP446363	C 495	18	1.1	5359	9	AF338357	AF338357	Pan trogl
C 423	18	1.1	912	6	A47120	C 496	18	1.1	5473	6	AR338769	AR338769	Sequence
C 424	18	1.1	912	8	AY088521	C 497	18	1.1	5760	9	HSMB08955	HSMB08955	Homo sapi
425	18	1.1	912	8	CQ812252	498	18	1.1	5924	8	MM4D7D	MM4D7D	Mucor muced
C 426	18	1.1	912	9	HSBTP2P35	499	18	1.1	6035	9	HSMB08873	HSMB08873	Sequence
427	18	1.1	932	5	BX950461	500	18	1.1	6222	10	AK122323	AK122323	Mus muscu
C 428	18	1.1	1024	6	AX790555	C 501	18	1.1	6382	1	AY550111	AY550111	Bacillus
C 429	18	1.1	1029	9	BC065250	C 502	18	1.1	6412	6	CQ598409	CQ598409	Sequence
C 430	18	1.1	1232	6	AR339181	C 503	18	1.1	6450	9	AY013288	AY013288	Homo sapi
C 431	18	1.1	1339	5	GGCBPAMR	504	18	1.1	6943	10	BC070449	BC070449	Mus muscu
C 432	18	1.1	1339	5	GGCBPAMR	505	18	1.1	7315	9	HSMB05565	HSMB05565	Homo sapi
433	18	1.1	1360	5	BC056300	506	18	1.1	7650	9	HSMB06134	HSMB06134	Homo sapi
434	18	1.1	1363	5	BC065891	507	18	1.1	10029	1	AE006872	AE006872	Sulfolobu
C 435	18	1.1	1460	9	BC047868	508	18	1.1	10157	6	CQ724045	CQ724045	Sequence
C 436	18	1.1	1539	6	AX066377	509	18	1.1	10172	6	AX333220	AX333220	Sequence
C 437	18	1.1	1543	6	BD092607	510	18	1.1	10172	9	HSU03272	HSU03272	Human fibro
C 438	18	1.1	1548	9	BC039857	C 511	18	1.1	10371	9	AY508451	AY508451	Sequence
C 439	18	1.1	1554	6	AX121655	C 512	18	1.1	10416	9	AY367067	AY367067	Gorilla g
C 440	18	1.1	1554	6	BD163782	C 513	18	1.1	10422	9	AY485422	AY485422	Actus ep.
C 441	18	1.1	1603	6	AX756597	C 514	18	1.1	10428	9	AY486114	AY486114	Cercopit
C 442	18	1.1	1634	10	AF314820	C 515	18	1.1	10431	9	AY485418	AY485418	Macaca fa
443	18	1.1	1743	9	AB089319	C 516	18	1.1	10434	9	AF509326	AF509326	Sequence
444	18	1.1	1747	6	BD136405	C 517	18	1.1	10434	9	AY367065	AY367065	Homo sapi
445	18	1.1	1748	6	AX827805	518	18	1.1	10434	9	AY367066	AY367066	Homo sapi
446	18	1.1	1748	10	RNU72349	C 519	18	1.1	10434	9	AY508452	AY508452	Pan trogl
447	18	1.1	1774	10	MMNORRIE	C 520	18	1.1	12019	1	AE011442	AE011442	Leptospir
C 448	18	1.1	2069	10	D45208	C 521	18	1.1	12186	1	AE000577	AE000577	Helicobac
C 449	18	1.1	2105	10	BC047133	522	18	1.1	13114	1	AE010650	AE010650	Fusobacte
450	18	1.1	2214	14	AY530556	C 523	18	1.1	14203	1	AE000948	AE000948	Archaeogl
451	18	1.1	2304	6	AX544437	C 524	18	1.1	16383	4	CMAS54052	CMAS54052	Caperea m
C 452	18	1.1	2334	6	BC039726	C 525	18	1.1	16390	4	BMY554051	BMY554051	Balaena m
C 453	18	1.1	2336	6	BC040439	C 526	18	1.1	16398	4	MTBPCG	MTBPCG	Balaenopter
454	18	1.1	2375	10	AY141038	C 527	18	1.1	16402	4	MTBMCG	MTBMCG	Balaenopter
C 455	18	1.1	2414	6	AX876687	C 528	18	1.1	16412	4	EROS54053	EROS54053	Eschricht
C 456	18	1.1	2414	6	BD156262	529	18	1.1	16829	4	RUMTGENOM	RUMTGENOM	Rhinoceros
C 457	18	1.1	2414	9	AK001411	C 530	18	1.1	16832	4	MTCSXX	MTCSXX	Cetacotheri

C 531	18	1.1	17734	4	LEU421471	604	18	1.1	82646	8	AB028611	AB028611 Arabidops
C 532	18	1.1	18954	9	AY339617	605	18	1.1	82944	9	AL354999	AL354999 Human DNA
C 533	18	1.1	28842	9	AL160158	C 606	18	1.1	84553	4	AC123538	AC123538 Sminthops
C 534	18	1.1	30788	3	AC078892	C 607	18	1.1	84649	2	AC013534	AC013534 Homo sapi
C 535	18	1.1	31930	3	U73331	C 608	18	1.1	85801	2	AL805909	AL805909 Human DNA
C 536	18	1.1	32202	3	U00050	C 609	18	1.1	85848	2	AL015733	AL015733 Homo sapi
C 537	18	1.1	32987	1	AB036666	C 610	18	1.1	86005	2	AC021938	AC021938 Homo sapi
C 538	18	1.1	33579	2	AC149419	C 611	18	1.1	86377	8	ATF17N18	ATF17N18 Arabidops
C 539	18	1.1	34518	9	AC107083	C 612	18	1.1	86630	8	AL592428	AL592428 Human DNA
C 540	18	1.1	34518	9	AC107083	C 613	18	1.1	86764	10	BX842611	BX842611 Mouse DNA
C 541	18	1.1	34796	5	BX005325	C 614	18	1.1	87575	8	AC011622	AC011622 Arabidops
C 542	18	1.1	35899	2	AC149378	C 615	18	1.1	87768	8	T22H22	AC005388 Sequence
C 543	18	1.1	36524	7	AF157835	C 616	18	1.1	88251	2	AC126325	AC126325 Homo sapi
C 544	18	1.1	37129	2	AC149360	C 617	18	1.1	88823	9	AL713965	AL713965 Human DNA
C 545	18	1.1	37702	2	AP001234	C 618	18	1.1	89177	9	AL356000	AL356000 Human DNA
C 546	18	1.1	38013	9	HS117A9B	C 619	18	1.1	89203	2	AC119504	AC119504 Rattus no
C 547	18	1.1	38881	2	AC149371	C 620	18	1.1	90011	9	AL360007	AL360007 Human DNA
C 548	18	1.1	38932	2	HSN38E12	C 621	18	1.1	90034	9	AP002012	AP002012 Homo sapi
C 549	18	1.1	39104	6	AX059483	C 622	18	1.1	90525	5	BX510955	BX510955 Zebrafish
C 550	18	1.1	40081	2	AC145669	C 623	18	1.1	90666	8	AC005662	AC005662 Arabidops
C 551	18	1.1	40302	3	CEC11G6	C 624	18	1.1	97095	2	AC141824	AC141824 Apis mell
C 552	18	1.1	41147	2	AC149423	C 625	18	1.1	97142	2	AC010439	AC010439 Homo sapi
C 553	18	1.1	41308	2	AC004196	C 626	18	1.1	98800	10	BX510362	BX510362 Mouse DNA
C 554	18	1.1	43722	2	AF020801	C 627	18	1.1	99416	9	AC105276	AC105276 Homo sapi
C 555	18	1.1	44548	9	AX695929	C 628	18	1.1	99999	9	AP000510	AP000510 Homo sapi
C 556	18	1.1	44577	6	AC020147	C 629	18	1.1	100382	9	AL162292	AL162292 Human DNA
C 557	18	1.1	48000	2	AC068821	C 630	18	1.1	102425	9	AC011363	AC011363 Homo sapi
C 558	18	1.1	50487	2	AC068821	C 631	18	1.1	102714	9	AP000692	AP000692 Homo sapi
C 559	18	1.1	52307	2	AC019584	C 632	18	1.1	102757	9	AL353698	AL353698 Human DNA
C 560	18	1.1	52358	2	HS27C10	C 633	18	1.1	102992	2	AL591863	AL591863 Homo sapi
C 561	18	1.1	54456	2	AL591047	C 634	18	1.1	103428	2	AC096435	AC096435 Homo sapi
C 562	18	1.1	55219	2	AC100542	C 635	18	1.1	103950	9	AC034235	AC034235 Homo sapi
C 563	18	1.1	58155	2	AC100949	C 636	18	1.1	104228	9	AL135917	AL135917 Human DNA
C 564	18	1.1	58179	2	AC090272	C 637	18	1.1	104485	10	AB114903	AB114903 Mus muscu
C 565	18	1.1	58536	2	AL161718	C 638	18	1.1	105499	9	AC093335	AC093335 Homo sapi
C 566	18	1.1	59012	2	HSABLGK2	C 639	18	1.1	106159	4	AC124041	AC124041 Arabidops
C 567	18	1.1	59932	2	AF020802	C 640	18	1.1	106248	5	AL928595	AL928595 Zebrafish
C 568	18	1.1	61946	2	AF020802	C 641	18	1.1	108175	9	AC068206	AC068206 Homo sapi
C 569	18	1.1	62370	2	AL451008	C 642	18	1.1	108651	9	AC034214	AC034214 Homo sapi
C 570	18	1.1	62377	2	AL360009	C 643	18	1.1	108700	9	AC131952	AC131952 Homo sapi
C 571	18	1.1	62544	2	AY339212	C 644	18	1.1	109296	2	AC083949	AC083949 Homo sapi
C 572	18	1.1	63090	2	AC087320	C 645	18	1.1	109345	2	AC019325	AC019325 Homo sapi
C 573	18	1.1	63633	2	AL139409	C 646	18	1.1	109432	2	AC019325	AC019325 Homo sapi
C 574	18	1.1	63894	2	AC140885	C 647	18	1.1	110000	1	AB000516	AB000516 Arabidops
C 575	18	1.1	64703	2	AC136718	C 648	18	1.1	110000	2	AC108442	AC108442 Mus muscu
C 576	18	1.1	65389	2	AY497017	C 649	18	1.1	110000	2	AC114782	AC114782 Homo sapi
C 577	18	1.1	65600	9	AY497013	C 650	18	1.1	110000	2	AC114782	AC114782 Homo sapi
C 578	18	1.1	66069	9	AY497016	C 651	18	1.1	110000	2	AC119592	AC119592 Homo sapi
C 579	18	1.1	66089	9	AY497014	C 652	18	1.1	110000	2	AC120236	AC120236 Homo sapi
C 580	18	1.1	68332	2	AC107155	C 653	18	1.1	110000	2	AC128782	AC128782 Homo sapi
C 581	18	1.1	68554	2	AC010416	C 654	18	1.1	110000	2	AC129424	AC129424 Homo sapi
C 582	18	1.1	68589	2	AC087682	C 655	18	1.1	110000	2	AC132794	AC132794 Homo sapi
C 583	18	1.1	68986	8	T22111	C 656	18	1.1	110000	2	AC141459	AC141459 Homo sapi
C 584	18	1.1	69017	2	HS41018	C 657	18	1.1	110000	2	AC142960	AC142960 Homo sapi
C 585	18	1.1	69093	2	AC134785	C 658	18	1.1	110000	2	AP006490	AP006490 Arabidops
C 586	18	1.1	69731	2	AC116014	C 659	18	1.1	110000	2	PFMAL791_06	PFMAL791_06 Arabidops
C 587	18	1.1	69745	2	AC114801	C 660	18	1.1	110000	8	CR380951	CR380951 Homo sapi
C 588	18	1.1	70642	2	AC099870	C 661	18	1.1	110000	8	CR382123	CR382123 Homo sapi
C 589	18	1.1	71091	2	AC106052	C 662	18	1.1	110000	8	CR382123	CR382123 Homo sapi
C 590	18	1.1	71179	2	AL136110	C 663	18	1.1	110391	10	AF390547	AF390547 Mus muscu
C 591	18	1.1	71927	2	AC024464	C 664	18	1.1	110494	8	AP004139	AP004139 Oryza sat
C 592	18	1.1	73218	2	HS209H1	C 665	18	1.1	112182	2	AC141177	AC141177 Rattus no
C 593	18	1.1	75621	9	BX247900	C 666	18	1.1	112266	8	AC093490	AC093490 Oryza sat
C 594	18	1.1	75688	5	AC149073	C 667	18	1.1	112560	9	HSJ513G18	HSJ513G18 Human DNA
C 595	18	1.1	75709	8	AB010693	C 668	18	1.1	112626	9	AC093748	AC093748 Homo sapi
C 596	18	1.1	76581	8	AL355304	C 669	18	1.1	113214	2	AC011344	AC011344 Homo sapi
C 597	18	1.1	77858	2	AL355304	C 670	18	1.1	113335	2	CNS08C72	CNS08C72 Oryza sat
C 598	18	1.1	80662	2	AL645929	C 671	18	1.1	113415	8	AP004860	AP004860 Oryza sat
C 599	18	1.1	81188	2	AP001128	C 672	18	1.1	114127	9	AC008683	AC008683 Homo sapi
C 600	18	1.1	81780	2	AL161440	C 673	18	1.1	114688	9	AC125437	AC125437 Homo sapi
C 601	18	1.1	82359	8	ATAC002342	C 674	18	1.1	114691	4	AC144636	AC144636 Arabidops
C 602	18	1.1	82422	9	AL138763	C 675	18	1.1	115224	4	AL356234	AL356234 Human DNA
C 603	18	1.1	82599	8	AP004498	C 676	18	1.1	115890	10	AC114412	AC114412 Mus muscu

677	18	1.1	116098	2	AC023867	Hom	sapi	AC023867	Hom	sapi	750	18	1.1	143088	9	AC005684	Hom	sapi	AC005684	Hom	sapi
678	18	1.1	117084	9	AL139247	Human	DNA	AL139247	Human	DNA	751	18	1.1	143841	9	AC008964	Hom	sapi	AC008964	Hom	sapi
679	18	1.1	117327	9	AL663093	Human	DNA	AL663093	Human	DNA	752	18	1.1	144116	10	AL671907	Hom	sapi	AL671907	Hom	sapi
680	18	1.1	117714	3	AC098797	Leishmani		AC098797	Leishmani		753	18	1.1	144136	2	AC012243	Hom	sapi	AC012243	Hom	sapi
681	18	1.1	119307	9	AC004134	Hom	sapi	AC004134	Hom	sapi	754	18	1.1	144234	2	AP002425	Hom	sapi	AP002425	Hom	sapi
682	18	1.1	119525	8	AP006366	Lotus	cor	AP006366	Lotus	cor	755	18	1.1	144279	2	AP001570	Hom	sapi	AP001570	Hom	sapi
683	18	1.1	119944	9	AC111162	Hom	sapi	AC111162	Hom	sapi	756	18	1.1	144348	2	AC016423	Hom	sapi	AC016423	Hom	sapi
684	18	1.1	120405	2	AC046147	Mus	muscu	AC046147	Mus	muscu	757	18	1.1	144709	2	AC012084	Rattus	no	AC120084	Rattus	no
685	18	1.1	120594	2	AC149264	Medicago		AC149264	Medicago		758	18	1.1	144924	9	HS056978	Hom	sapi	AL050403	Human	DNA
686	18	1.1	121207	8	AP006077	Lotus	cor	AP006077	Lotus	cor	759	18	1.1	144941	9	AL591848	Human	DNA	AL591848	Human	DNA
687	18	1.1	123842	2	AC129474	Hom	sapi	AC129474	Hom	sapi	760	18	1.1	145270	10	AC140366	Hom	sapi	AC140366	Mus	muscu
688	18	1.1	123369	2	AC025170	Hom	sapi	AC025170	Hom	sapi	761	18	1.1	145383	2	AC116816	Hom	sapi	AC116816	Mus	muscu
689	18	1.1	124329	2	AC144420	Rattus	no	AC144420	Rattus	no	762	18	1.1	145859	2	AC116336	Hom	sapi	AC116336	Hom	sapi
690	18	1.1	124661	2	AC127541	Hom	sapi	AC127541	Hom	sapi	763	18	1.1	146154	2	AP004400	Oryza	sat	AP004400	Oryza	sat
691	18	1.1	125304	9	AC008044	Hom	sapi	AC008044	Hom	sapi	764	18	1.1	146366	9	AL627231	Human	DNA	AL627231	Human	DNA
692	18	1.1	125502	8	ATT41220	Hom	sapi	AL023094	Arabidops		765	18	1.1	146671	2	AC093810	Hom	sapi	AC093810	Hom	sapi
693	18	1.1	126222	2	AL844492	Hom	sapi	AL844492	Hom	sapi	766	18	1.1	146691	2	AP002402	Hom	sapi	AP002402	Hom	sapi
694	18	1.1	126394	9	AC109998	Hom	sapi	AC109998	Hom	sapi	767	18	1.1	146916	2	AC026931	Hom	sapi	AC026931	Hom	sapi
695	18	1.1	127526	9	AC006315	Hom	sapi	AC006315	Hom	sapi	768	18	1.1	147109	2	AL591043	Human	DNA	AL591043	Human	DNA
696	18	1.1	129109	9	AL390239	Human	DNA	AL390239	Human	DNA	769	18	1.1	147367	2	AC073966	Hom	sapi	AC073966	Hom	sapi
697	18	1.1	129257	2	AC148368	Meleagris		AC148368	Meleagris		770	18	1.1	147367	2	AC073966	Hom	sapi	AC073966	Hom	sapi
698	18	1.1	129361	9	AL603789	Human	DNA	AL603789	Human	DNA	771	18	1.1	147859	2	AC092993	Hom	sapi	AC092993	Hom	sapi
699	18	1.1	129782	5	BX120005	Zebrafish		BX120005	Zebrafish		772	18	1.1	147940	2	AC026913	Hom	sapi	AC026913	Hom	sapi
700	18	1.1	129880	9	AC104334	Hom	sapi	AC104334	Hom	sapi	773	18	1.1	148345	2	AL592151	Human	DNA	AL592151	Human	DNA
701	18	1.1	130307	9	AC113355	Hom	sapi	AC113355	Hom	sapi	774	18	1.1	148491	8	AP005926	Oryza	sat	AP005926	Oryza	sat
702	18	1.1	130870	10	AL731775	Mouse	DNA	AL731775	Mouse	DNA	775	18	1.1	149453	10	AC084109	Hom	sapi	AC084109	Mus	muscu
703	18	1.1	131312	9	AC008456	Hom	sapi	AC008456	Hom	sapi	776	18	1.1	150021	5	BX088691	Zebrafish		BX088691	Zebrafish	
704	18	1.1	131387	10	AC079440	Mus	muscu	AC079440	Mus	muscu	777	18	1.1	150145	2	AC069216	Hom	sapi	AC069216	Hom	sapi
705	18	1.1	131489	9	AC093505	Hom	sapi	AC093505	Hom	sapi	778	18	1.1	150159	2	AC018791	Hom	sapi	AC018791	Hom	sapi
706	18	1.1	131637	9	CNS01DUC	Human	chr	AL133239	Human	chr	779	18	1.1	150399	2	AC009369	Hom	sapi	AC009369	Drosophi	
707	18	1.1	131743	8	AC004561	Arabidops		AC004561	Arabidops		780	18	1.1	150565	2	BX927078	Danio	rer	BX927078	Danio	rer
708	18	1.1	132191	9	AC090349	Hom	sapi	AC090349	Hom	sapi	781	18	1.1	150680	2	AC090894	Hom	sapi	AC090894	Hom	sapi
709	18	1.1	132301	2	AC129954	Bos	tauru	AC129954	Bos	tauru	782	18	1.1	150817	2	AC021762	Hom	sapi	AC021762	Hom	sapi
710	18	1.1	132492	9	AC007616	Hom	sapi	AC007616	Hom	sapi	783	18	1.1	150879	2	AC074017	Hom	sapi	AC074017	Hom	sapi
711	18	1.1	132585	9	AC131947	Hom	sapi	AC131947	Hom	sapi	784	18	1.1	151235	9	AC090936	Hom	sapi	AC090936	Hom	sapi
712	18	1.1	132647	8	AC073393	Oryza	sat	AC073393	Oryza	sat	785	18	1.1	151325	9	AC074363	Hom	sapi	AC074363	Hom	sapi
713	18	1.1	132867	9	AC004601	Human	11p	AC004601	Human	11p	786	18	1.1	151446	5	AL627088	Danio	rer	AL627088	Zebrafish	
714	18	1.1	132953	9	AC003015	Human	BAC	AC003015	Human	BAC	787	18	1.1	151708	2	AL929460	Danio	rer	AL929460	Danio	rer
715	18	1.1	133028	8	AP003447	Oryza	sat	AP003447	Oryza	sat	788	18	1.1	151784	2	AC138664	Mus	muscu	AC138664	Mus	muscu
716	18	1.1	133563	8	AC099481	Hom	sapi	AC099481	Hom	sapi	789	18	1.1	151828	8	AC018632	Hom	sapi	AC018632	Genomic S	
717	18	1.1	133843	8	AC003981	Genomic s		AC003981	Genomic s		790	18	1.1	151847	2	AC022792	Hom	sapi	AC022792	Hom	sapi
718	18	1.1	133910	10	AL929253	Mouse	DNA	AL929253	Mouse	DNA	791	18	1.1	151921	10	AL845499	Mouse	DNA	AL845499	Mouse	DNA
719	18	1.1	134369	9	AC104825	Hom	sapi	AC104825	Hom	sapi	792	18	1.1	152181	9	AL391869	Human	DNA	AL391869	Human	DNA
720	18	1.1	135079	9	HS0J70A9	Human	DNA	AL121788	Human	DNA	793	18	1.1	152336	9	AP004714	Hom	sapi	AP004714	Hom	sapi
721	18	1.1	135396	9	BX927139	Hom	sapi	BX927139	Hom	sapi	794	18	1.1	152787	2	AC026623	Oryza	sat	AC026623	Oryza	sat
722	18	1.1	135505	9	AC004477	Hom	sapi	AC004477	Hom	sapi	795	18	1.1	153064	8	CNS08CAL	Hom	sapi	AC022044	Hom	sapi
723	18	1.1	135545	10	MMHC213L3	Mus	muscu	AF109905	Mus	muscu	796	18	1.1	153096	2	AC022044	Hom	sapi	AC022044	Hom	sapi
724	18	1.1	135726	8	AC147498	Medicago		AC147498	Medicago		797	18	1.1	153295	2	AC060758	Hom	sapi	AC060758	Hom	sapi
725	18	1.1	136544	9	AC127033	Hom	sapi	AC127033	Hom	sapi	798	18	1.1	153365	2	AC142443	Hom	sapi	AC142443	Hom	sapi
726	18	1.1	137554	2	AC127618	Rattus	no	AC127618	Rattus	no	799	18	1.1	153605	8	AC147764	Daeypus	n	AC147764	Daeypus	n
727	18	1.1	137557	9	AC005909	Hom	sapi	AC005909	Hom	sapi	800	18	1.1	153743	8	AP005108	Oryza	sat	AP005108	Oryza	sat
728	18	1.1	138041	9	CNS01DUI	Hom	sapi	AL133245	BAC	seque	801	18	1.1	153897	5	AL928656	Zebrafish		AL928656	Zebrafish	
729	18	1.1	138586	8	AC144726	Medicago		AC144726	Medicago		802	18	1.1	154085	2	BX537124	Danio	rer	BX537124	Danio	rer
730	18	1.1	138909	9	CNS01DMS	BAC	seque	AL121653	BAC	seque	803	18	1.1	154285	9	AL606923	Human	DNA	AL606923	Human	DNA
731	18	1.1	138951	2	AC115068	Mus	muscu	AL122161	Human	DNA	804	18	1.1	154315	9	AP005380	Hom	sapi	AP005380	Hom	sapi
732	18	1.1	139444	2	HS380C13	Hom	sapi	AL022161	Human	DNA	805	18	1.1	154594	9	AL161722	Hom	sapi	AL161722	Hom	sapi
733	18	1.1	139469	2	AC143350	Hom	sapi	AL049652	Human	DNA	806	18	1.1	154713	2	AC144335	Hom	sapi	AC144335	Hom	sapi
734	18	1.1	139512	9	HSJ1169J3	Hom	sapi	AL049652	Human	DNA	807	18	1.1	154765	9	AC013361	Hom	sapi	AC013361	Hom	sapi
735	18	1.1	139558	10	AL929129	Hom	sapi	AL929129	Hom	sapi	808	18	1.1	155198	2	AL537553	Hom	sapi	AL537553	Hom	sapi
736	18	1.1	139653	2	AP005890	Oryza	sat	AP005890	Oryza	sat	809	18	1.1	155199	2	HS616B8	Hom	sapi	HS616B8	Hom	sapi
737	18	1.1	139796	8	AP005782	Oryza	sat	AP005782	Oryza	sat	810	18	1.1	155413	2	AC068304	Hom	sapi	AC068304	Hom	sapi
738	18	1.1	141073	8	AC105108	Hom	sapi	AC105108	Hom	sapi	811	18	1.1	155613	2	AC149867	Papio	anu	AC149867	Papio	anu
739	18	1.1	141275	8	AP003141	Oryza	sat	AP003141	Oryza	sat	812	18	1.1	155868	9	AC016764	Hom	sapi	AC016764	Hom	sapi
740	18	1.1	141368	8	AC134341	Oryza	sat	AC134341	Oryza	sat	813	18	1.1	155892	9	AL353809	Human	DNA	AL353809	Human	DNA
741	18	1.1	141401	10	AL844585	Mouse	DNA	AL844585	Mouse	DNA	814	18	1.1	156193	10	AL669907	Mouse	DNA	AL669907	Mouse	DNA
742	18	1.1	141467	9	AC016204	Hom	sapi	AC016204	Hom	sapi	815	18	1.1	156272	9	AL669830	Human	DNA	AL669830	Human	DNA
743	18	1.1	141767	9	BS000199	Pan	trogl	BS000199	Pan	trogl	816	18	1.1	156432	9	HS581F7	Hom	sapi	HS581F7	Hom	sapi
744	18	1.1	141772	2	BX571792	Danio	rer	BX571792	Danio	rer	817	18									

823	18	1.1	157402	2	AC034161	AC034161 Homo sapi	896	18	1.1	166077	5	BX470143	BX470143 Zebrafish
824	18	1.1	157410	2	AC143922	AC143922 Xecopa mu	897	18	1.1	166108	2	AC114304	AC114304 Homo sapi
825	18	1.1	157592	2	AC145798	AC145798 Xenopus t	898	18	1.1	166219	9	AC003084	AC003084 Homo sapi
826	18	1.1	158072	2	AC053533	AC053533 Homo sapi	899	18	1.1	166323	2	AC142439	AC142439 Rattus no
827	18	1.1	158168	2	AC142544	AC142544 Homo sapi	900	18	1.1	166655	9	AC104161	AC104161 Homo sapi
828	18	1.1	158180	2	AC100781	AC100781 Homo sapi	901	18	1.1	166763	2	AC112941	AC112941 Mus muscu
829	18	1.1	158224	5	BX233886	BX233886 Zebrafish	902	18	1.1	167140	5	BX248985	BX248985 Zebrafish
830	18	1.1	158229	2	AC133596	AC133596 Homo sapi	903	18	1.1	167683	2	AC079251	AC079251 Homo sapi
831	18	1.1	158508	9	AC107622	AC107622 Homo sapi	904	18	1.1	167834	2	AC148164	AC148164 Zee maye
832	18	1.1	158595	2	AC010614	AC010614 Homo sapi	905	18	1.1	168108	2	AC104119	AC104119 Homo sapi
833	18	1.1	158785	2	AC027699	AC027699 Homo sapi	906	18	1.1	168127	10	AC117243	AC117243 Mus muscu
834	18	1.1	158816	2	AC009368	AC009368 Drosophill	907	18	1.1	168139	2	AC118638	AC118638 Mus muscu
835	18	1.1	159128	10	AL928557	AL928557 Mouse DNA	908	18	1.1	168177	2	AC023914	AC023914 Homo sapi
836	18	1.1	159322	2	BX57240	BX57240 Dantio rer	909	18	1.1	168339	2	BX649454	BX649454 Dantio rer
837	18	1.1	159480	2	AC021843	AC021843 Homo sapi	910	18	1.1	168360	4	AC145183	AC145183 Macropus
838	18	1.1	159577	2	AC080060	AC080060 Homo sapi	911	18	1.1	168406	2	AC090770	AC090770 Homo sapi
839	18	1.1	159723	2	AC021862	AC021862 Homo sapi	912	18	1.1	168476	2	AC011260	AC011260 Homo sapi
840	18	1.1	160379	5	BX233558	BX233558 Zebrafish	913	18	1.1	168535	8	AP006235	AP006235 Oryza sat
841	18	1.1	160390	2	AC129676	AC129676 Homo sapi	914	18	1.1	169082	10	AC130538	AC130538 Mus muscu
842	18	1.1	160472	2	AC080140	AC080140 Mus muscu	915	18	1.1	169155	5	BX088685	BX088685 Zebrafish
843	18	1.1	160583	2	AC010968	AC010968 Homo sapi	916	18	1.1	169207	9	AC007490	AC007490 Homo sapi
844	18	1.1	160869	2	AC026378	AC026378 Mus muscu	917	18	1.1	169365	2	AC023341	AC023341 Homo sapi
845	18	1.1	160918	2	AC069196	AC069196 Homo sapi	918	18	1.1	169571	2	AC020687	AC020687 Homo sapi
846	18	1.1	161136	2	AC142078	AC142078 Homo sapi	919	18	1.1	169746	2	AC108911	AC108911 Mus muscu
847	18	1.1	161653	2	AC026619	AC026619 Homo sapi	920	18	1.1	169753	2	AC087506	AC087506 Homo sapi
848	18	1.1	161672	2	AC136667	AC136667 Rattus no	921	18	1.1	170219	2	AP001378	AP001378 Homo sapi
849	18	1.1	161685	2	AC103901	AC103901 Carls fam	922	18	1.1	170337	2	AP001378	AP001378 Homo sapi
850	18	1.1	161754	3	AC007451	AC007451 Drosophill	923	18	1.1	170432	2	AC023322	AC023322 Homo sapi
851	18	1.1	161865	8	AP005912	AP005912 Oryza sat	924	18	1.1	170490	2	AC022042	AC022042 Homo sapi
852	18	1.1	161883	2	AC025825	AC025825 Oryza sat	925	18	1.1	170522	9	AL138708	AL138708 Homo sapi
853	18	1.1	161920	2	AC025169	AC025169 Homo sapi	926	18	1.1	170741	10	AC130212	AC130212 Mus muscu
854	18	1.1	162088	2	AC069479	AC069479 Homo sapi	927	18	1.1	170745	2	AC120835	AC120835 Rattus no
855	18	1.1	162115	5	BX569788	BX569788 Zebrafish	928	18	1.1	170780	9	CNS01RM7	CNS01RM7 Homo sapi
856	18	1.1	162352	2	AC093977	AC093977 Homo sapi	929	18	1.1	170781	2	AC013473	AC013473 Homo sapi
857	18	1.1	162352	2	AC150523	AC150523 Bos tauru	930	18	1.1	170893	2	CR626910	CR626910 Dantio rer
858	18	1.1	162355	2	AC126015	AC126015 Medicago	931	18	1.1	171196	2	AP001369	AP001369 Homo sapi
859	18	1.1	162489	2	AP001572	AP001572 Homo sapi	932	18	1.1	171430	2	AC110599	AC110599 Homo sapi
860	18	1.1	162522	2	AC021014	AC021014 Homo sapi	933	18	1.1	171501	9	AL359704	AL359704 Homo sapi
861	18	1.1	162691	2	AC031523	AC031523 Homo sapi	934	18	1.1	171653	9	AC080162	AC080162 Homo sapi
862	18	1.1	162784	9	AC011197	AC011197 Homo sapi	935	18	1.1	171850	2	AC024405	AC024405 Homo sapi
863	18	1.1	162881	9	AC022174	AC022174 Homo sapi	936	18	1.1	171941	2	AC026531	AC026531 Homo sapi
864	18	1.1	162964	9	AC011939	AC011939 Homo sapi	937	18	1.1	172290	2	AC021728	AC021728 Homo sapi
865	18	1.1	163050	2	AC020696	AC020696 Homo sapi	938	18	1.1	172298	2	AC009556	AC009556 Homo sapi
866	18	1.1	163316	9	AL161420	AL161420 Homo sapi	939	18	1.1	172378	2	AC021696	AC021696 Homo sapi
867	18	1.1	163373	2	AC024263	AC024263 Homo sapi	940	18	1.1	172745	9	AC010591	AC010591 Homo sapi
868	18	1.1	163389	2	AL589765	AL589765 Homo sapi	941	18	1.1	173180	2	AC147981	AC147981 Rattus no
869	18	1.1	163419	5	BX323847	BX323847 Zebrafish	942	18	1.1	173805	2	AL606966	AL606966 Homo sapi
870	18	1.1	163776	2	AC109289	AC109289 Mus muscu	943	18	1.1	173816	2	AC141887	AC141887 Mus muscu
871	18	1.1	163788	2	AC018996	AC018996 Homo sapi	944	18	1.1	174176	5	AL772340	AL772340 Zebrafish
872	18	1.1	164018	9	AL354868	AL354868 Homo sapi	945	18	1.1	174239	2	AC073830	AC073830 Homo sapi
873	18	1.1	164219	5	BX005205	BX005205 Zebrafish	946	18	1.1	174304	9	AL450327	AL450327 Homo sapi
874	18	1.1	164454	9	AC093431	AC093431 Homo sapi	947	18	1.1	174504	2	AC015964	AC015964 Homo sapi
875	18	1.1	164514	9	CNS01RMV	CNS01RMV Homo sapi	948	18	1.1	174711	2	AC026639	AC026639 Homo sapi
876	18	1.1	164569	8	OSJN00072	OSJN00072 Homo sapi	949	18	1.1	174736	9	AC132924	AC132924 Homo sapi
877	18	1.1	164589	2	AC026043	AC026043 Homo sapi	950	18	1.1	174799	2	AC142548	AC142548 Homo sapi
878	18	1.1	164820	9	AC092598	AC092598 Homo sapi	951	18	1.1	175109	2	AC124279	AC124279 Homo sapi
879	18	1.1	164836	2	AC117341	AC117341 Rattus no	952	18	1.1	175132	9	AL359641	AL359641 Homo sapi
880	18	1.1	164933	2	AC149122	AC149122 Rattus no	953	18	1.1	175177	2	AC147852	AC147852 Homo sapi
881	18	1.1	164736	2	AC117341	AC117341 Rattus no	954	18	1.1	175368	2	CNS01DMF	CNS01DMF Homo sapi
882	18	1.1	164798	9	AC092598	AC092598 Homo sapi	955	18	1.1	175378	2	AC113179	AC113179 Mus muscu
883	18	1.1	164820	9	AL627443	AL627443 Homo sapi	956	18	1.1	175378	2	AC115049	AC115049 Bos tauru
884	18	1.1	164872	9	AC009567	AC009567 Homo sapi	957	18	1.1	175495	5	BX001050	BX001050 Zebrafish
885	18	1.1	165073	2	AC148684	AC148684 Macaca mu	958	18	1.1	175543	2	AC073378	AC073378 Homo sapi
886	18	1.1	165168	2	AC148167	AC148167 Zee maye	959	18	1.1	175555	8	OSJN00237	OSJN00237 Homo sapi
887	18	1.1	165287	2	AC090599	AC090599 Homo sapi	960	18	1.1	175609	2	AC024663	AC024663 Homo sapi
888	18	1.1	165350	8	AC150788	AC150788 Oryza sat	961	18	1.1	175631	9	AC023511	AC023511 Homo sapi
889	18	1.1	165378	8	AC129805	AC129805 Homo sapi	962	18	1.1	175832	2	AC023080	AC023080 Homo sapi
890	18	1.1	165488	10	AL807810	AL807810 Mouse DNA	963	18	1.1	175835	2	AC024074	AC024074 Homo sapi
891	18	1.1	165527	2	AC109468	AC109468 Homo sapi	964	18	1.1	176249	2	AC069497	AC069497 Homo sapi
892	18	1.1	165570	2	AC007994	AC007994 Mus muscu	965	18	1.1	176268	5	AL954175	AL954175 Zebrafish
893	18	1.1	165701	8	AP004357	AP004357 Oryza sat	966	18	1.1	176466	9	AL161733	AL161733 Homo sapi
894	18	1.1	165854	9	AC073043	AC073043 Homo sapi	967	18	1.1	176555	9	AL366579	AL366579 Homo sapi
895	18	1.1	166054	9	AC069550	AC069550 Sequence	968	18	1.1	176565	2	AL136106	AL136106 Homo sapi

969	18	1.1	176757	4	AC095025	AC095025 Sus scrofa
970	18	1.1	176932	9	HS121G13	286062 Human DNA s
971	18	1.1	177003	9	AL590095	AL590095 Human DNA
972	18	1.1	177018	2	AC103584	AC103584 Bos taurus
973	18	1.1	177098	10	AL731695	AL731695 Mouse DNA
974	18	1.1	177171	2	AC128176	AC128176 Rattus no
975	18	1.1	177363	9	AC073856	AC073856 Homo sapi
976	18	1.1	177471	9	AC007446	AC007446 Homo sapi
977	18	1.1	177627	2	AC148261	AC148261 Callithrix
978	18	1.1	177664	2	AC015749	AC015749 Homo sapi
979	18	1.1	177914	2	AC080141	AC080141 Mus muscu
980	18	1.1	178171	2	AC026561	AC026561 Homo sapi
981	18	1.1	178502	10	AC120397	AC120397 Mus muscu
982	18	1.1	178676	2	AC026965	AC026965 Homo sapi
983	18	1.1	178688	2	AL713893	AL713893 Homo sapi
984	18	1.1	178896	8	AP005709	AP005709 Oryza sat
985	18	1.1	179030	9	AC019254	AC019254 Homo sapi
986	18	1.1	179085	9	AC011611	AC011611 Homo sapi
987	18	1.1	179138	2	AC121439	AC121439 Rattus no
988	18	1.1	179344	2	AC147979	AC147979 Rattus no
989	18	1.1	179358	9	AP001496	AP001496 Homo sapi
990	18	1.1	179503	2	AC140790	AC140790 Gallus ga
991	18	1.1	179773	2	AC116041	AC116041 Papio ham
992	18	1.1	179964	9	AL606527	AL606527 Human DNA
993	18	1.1	180000	1	AF322012	AF322012 Bradyrhiz
994	18	1.1	180137	2	BX957257	BX957257 Danio rer
995	18	1.1	180192	2	AC058810	AC058810 Homo sapi
996	18	1.1	180233	9	AC011767	AC011767 Homo sapi
997	18	1.1	180398	2	AC140262	AC140262 Mus muscu
998	18	1.1	180526	2	AC136083	AC136083 Rattus no
999	18	1.1	180793	2	AC064812	AC064812 Homo sapi
1000	18	1.1	181058	2	AC068118	AC068118 Homo sapi

ALIGNMENTS

RESULT 1
AX090311
LOCUS AX090311
DEFINITION Sequence 4 from Patent WO0116308.
ACCESSION AX090311
VERSION AX090311.1 GI:13444180
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
AUTHORS Laessle, M. and van Eenennaam, A.
TITLE Plant sterol acyltransferases
JOURNAL Patent: WO 0116308-A 4 08-MAR-2001;
MONSANTO COMPANY (US)
FEATURES
Source location/Qualifiers

1..1641
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN

Query Match 100.0%; Score 1641; DB 6; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	481	CCAACCAATTTGGAAGCGTGACCTTTACTTTCACAAAGCTCAAGTTGAACT	540
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DB	781	CGTTGTTGTCATATCTTTTGGTGTGATGATGATGATGATGATGATGATGATGATGAT	840
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DB	841	AAAGGTATTAACATCTGGAACGATTTTCTGGGGGTGCTGCAAAAGAAATTAAGGC	900
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DB	901	GATATCACTGTATGAAAGAGAAATATCAATCAAAATATTTGGCTGGCCGACAAATAT	960
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DEFINITION Novel class enzyme in biosynthesis pathway of triacylglycerol
production and recombinant DNA molecule encoding the enzyme.
ACCESSION BD271623
VERSION BD271623.1 GI:33081391
KEYWORDS JP 2002541783-A/8.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

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REFERENCE 1 (bases 1 to 3896)
AUTHORS Dahlqvist, A., Stahl, U., Lenman, M., Banas, A., Ronne, H. and Stymne, S.
TITLE Novel class enzyme in biosynthesis pathway of triacylglycerol
production and recombinant DNA molecule encoding the enzyme
JOURNAL BASF PLANT SCIENCE GMBH
COMMENT OS Arabidopsis thaliana (thale cress)
PN JP 2002541783-A/8
PD 10-DEC-2002
PR 28-MAR-2000 JP 2000609586
PR 01-APR-1999 EP 99106656.4, 10-JUN-1999 EP 99111321.8 PR
07-FEB-2000 US 60/180687
PI ANDERS DAHLQVIST, ULF STAHL, MARIT LENMAN, ANTONI BANAS PI
, HANS RONNE, STEN STYME
PC C12N5/09, A01H5/00, C12N1/19, C12N5/10, C12N9/10, C12P7/64// PC
(C12P7/64, C12R1:645), (C12P7/64, C12R1:91), C12N5/00, C12N5/00 CC
Novel class enzyme in biosynthesis pathway
of triacylglycerol
CC production
CC and recombinant DNA molecule encoding the enzyme FH Key
FT source 1. .3896
Location/Qualifiers
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Query Match 14.8%; Score 243; DB 6; Length 3896;
Best Local Similarity 100.0%; Pred. No. 1.2e-130; Indels 0; Gaps 0;
Matches 243; Conservative 0; Mismatches 0;

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DEFINITION Novel class enzyme in biosynthesis pathway of triacylglycerol
production and recombinant DNA molecule encoding the enzyme.
ACCESSION BD271633
VERSION BD271633.1 GI:33081401
KEYWORDS JP 2002541783-A/18.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

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REFERENCE 1 (bases 1 to 3896)
AUTHORS Dahlqvist, A., Stahl, U., Lenman, M., Banas, A., Ronne, H. and Stymne, S.
TITLE Novel class enzyme in biosynthesis pathway of triacylglycerol
production and recombinant DNA molecule encoding the enzyme
JOURNAL BASF PLANT SCIENCE GMBH
COMMENT OS Arabidopsis thaliana (thale cress)
PN JP 2002541783-A/18
PD 10-DEC-2002
PR 28-MAR-2000 JP 2000609586
PR 01-APR-1999 EP 99106656.4, 10-JUN-1999 EP 99111321.8 PR
07-FEB-2000 US 60/180687
PI ANDERS DAHLQVIST, ULF STAHL, MARIT LENMAN, ANTONI BANAS PI
, HANS RONNE, STEN STYME
PC C12N5/09, A01H5/00, C12N1/19, C12N5/10, C12N9/10, C12P7/64// PC
(C12P7/64, C12R1:645), (C12P7/64, C12R1:91), C12N5/00, C12N5/00 CC
Novel class enzyme in biosynthesis pathway
of triacylglycerol
CC production
CC and recombinant DNA molecule encoding the enzyme FH Key
FT source 1. .3896
Location/Qualifiers
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cress) /organism='Arabidopsis thaliana (thale FT

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Query Match 14.8%; Score 243; DB 6; Length 3896;

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Best Local Similarity 100.0%; Pred. No. 1,2e-130;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 AAG 243
DB 241 AAG 243

RESULT 4
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LOCUS AX037587
DEFINITION Sequence 11 from Patent WO0060095.
ACCESSION AX037587
VERSION AX037587.1 GI:11227006
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 Banaas,A., Stahl,U., Styenne,S., Lenman,M., Ronne,H. and Dahlqvist,A.
A new class of enzymes in the biosynthetic pathway for the
production of triacylglycerol and recombinant dna molecules
encoding these enzymes
Patent: WO 0060095-A 11 12-OCT-2000;
BASF PLANT SCIENCE GMBH (DE) ; BANAS ANTONI (PL) ; STAHL Ulf (SE) ;
STYENNE STEN (SE) ; LENMAN MARIT (SE) ; RONNE HANS (SE) ; DAHLQVIST
ANDERS (SE)

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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1,2e-130;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 241 AAG 243

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DEFINITION Sequence 30 from Patent WO0060095.
ACCESSION AX037606
VERSION AX037606.1 GI:11227020
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 Banaas,A., Stahl,U., Styenne,S., Lenman,M., Ronne,H. and Dahlqvist,A.
A new class of enzymes in the biosynthetic pathway for the
production of triacylglycerol and recombinant dna molecules
encoding these enzymes
Patent: WO 0060095-A 30 12-OCT-2000;
BASF PLANT SCIENCE GMBH (DE) ; BANAS ANTONI (PL) ; STAHL Ulf (SE) ;
STYENNE STEN (SE) ; LENMAN MARIT (SE) ; RONNE HANS (SE) ; DAHLQVIST
ANDERS (SE)

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source Location/Qualifiers
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Query Match 14.8%; Score 243; DB 6; Length 3896;
Best Local Similarity 100.0%; Pred. No. 1,2e-130;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CTATCGGGTATATATATTCGCGGATTTGGCTGAGACGCGCTACGACCGGTGCTATCTCTT 180
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DB 241 AAG 243

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LOCUS AC003027
DEFINITION Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence,
complete sequence.
ACCESSION AC003027
VERSION AC003027.1 GI:4079614
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 119914)
Federpiehl,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,B., Dunn,P.,

JOURNAL REFERENCE AUTHORS	2 (bases 1 to 119914) Federapfel,N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R., Au,M., Araujo,R., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y., Oji,O., Osborne,B.I., Shim,P., Sun,H., Tortum,M., Votetskaja,V., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
TITLE JOURNAL	Direct Submission Submitted (22-OCT-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo Alto, CA 94304, USA
REFERENCE AUTHORS	3 (bases 1 to 119914) Federapfel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizier,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremetskaja,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Tortum,M., Votetskaja,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
TITLE JOURNAL	Direct Submission Submitted (30-DEC-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
REFERENCE AUTHORS	4 (bases 1 to 119914) Federapfel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizier,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremetskaja,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Tortum,M., Votetskaja,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
TITLE JOURNAL	Direct Submission Submitted (30-JUN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT	On Dec 30, 1998 this sequence version replaced gi:2734094. 'bases 1-9262 of clone F21M1 overlap with bases 68998-78259 of 'TAMU' BAC clone F20D22 (AC002411) and bases 11955-119914 of clone F21M1 overlap with bases 1-389 of 'TAMU' BAC clone F21B7 (AC002560). e-mail for correspondence: arab@sequence.stanford.edu Genes with similarity to proteins in the databases are described as 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Graft (Informatics Group, Oak Ridge National Laboratory, http://compro.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://genomic.stanford.edu/~chris/GENSCAN.html), Fexa (V Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html). Location/Qualifiers
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 MDVEYFPLCGHNSVYKPNKSGHRSAPLEKIPALCEISLEQPAFKEVLEISCRG
 SALSGSKCKMESLAVRNPAITISRYNVPYTHVIAISDDEKGACTRILKVLGILNGKMK


```

11NAAAMKASLKAQPVDEBPFIQIDTQCGQDQPKTKARLAETNKRKLPBGLKPYFF
GDFYKGYKEDLQNLKVAAGTILNTEDELKGESSNNVNDQSSSIWYNIDPFGCAL
GEEVYIIWQANDAEALASQTSRLVHTWLESJAGYKXLPVIG"
/gene="P21M11.5"
20752..24647
/join(20752..20994,21362..21497,21596..21740,21825..21994,
22102..22178,22542..22758,22920..23066,23343..23442,
23599..23693,24021..24072,24227..24298,24441..24647)
/gene="P21M11.5"
/note="Hypothetical protein"
/codon_start=1
/protein_id="AADI0668.1"
/db_xref="GI:4204287"
/translation="MGANSKSVTASFTVIAVFLICGRTAVDEDETFEHDYSLGCI
IIPGASTQLRAMSILDCPYTPDENPLDLVMDITKLASVNCMFKCMVADPYNQT
HPEKSRDPSGLSAITELDPGITYGPISTVWKEMKMCVEFGEANAIVAVPYDMRS
PTKEERDLVPHKILTEPRLKLRGSPSIFPAISMGNVRYFLEMRLBIAEPHYL
KMLDQHIAVFAVGAFLIGSVEATKSTLSGTPGLPVSEGGRTALLINSFASLMLMP
SKNCKDNTFWTHFSGGAAXKDKRYHCDDEEYSGSKSGMTNIIINIEPSTARELA
DGTLPKALIEDYDPSKRMHLQKRYVPEFVIRNTAHRSLAGFLVHDDPVFNFLTPA
BRPIKVNFCIYGALHKTVEGYFAPSGKPPDMWITDIIYETEGSLVSSGTVVG
NAGPITGDETVPHSLSWCKMGLGPKVNIWAPQILGKIKQCEHDSGVHVELAND
HEHGSDIANTTKAPRVKYTEFEDESEIPEKRTAVMELDKSGY"
27777..28734
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27777..28734
/gene="P21M11.6"
28007..28465
/gene="P21M11.6"
/note="Unknown protein; location of ESTs 20312477,
gb|H76794 and 203124XP, gb|AA605510"
/codon_start=1
/protein_id="AADI0670.1"
/db_xref="GI:4204289"
/translation="MNTKTMRLPPRRVLTADKRERDAFISVTDNPEIAKPPSPPP
KLVPVPVPIKSSSTAABRIGSNQMLAGLSEHYLTGTLFGEOMNORABAESS
KIKPSHTVEPBECEPKRKYREVANLIRSDGQILPGIVNPAQLARFLKL"
complement(29264..32033)
/gene="P21M11.7"
complement(join(29264..31015,31312..31414,31484..31587,

Query Match          14.8%; Score 243; DB 8; Length 119914;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGGAGCGCAATTCGAATCAGTAACGGCTTCCTCACCGTCATCGCCGTTTTTCTTG 60
Db      20752 ATGGAGCGCAATTCGAATCAGTAACGGCTTCCTCACCGTCATCGCCGTTTTTCTTG 20811

Qy      61  ATTTGCGGTGGCCGAACCTGCGGTGAGATGAGACCGAGTTTCACGGCGACTCTCGAAG 120
Db      20812 ATTTGCGGTGGCCGAACCTGCGGTGAGATGAGACCGAGTTTCACGGCGACTCTCGAAG 20871

Qy      121 CTATCGGGTATTAATATCCGGGATTTGGCTGACGAGCTACGAGCGGTGATCTCTT 180
Db      20872 CTATCGGGTATTAATATCCGGGATTTGGCTGACGAGCTACGAGCGGTGATCTCTT 20931

Qy      181 GACTGTCCATACACTCCGTTGACTTCATCCGCTCGACCTCGATGCTAGACACCACT 240
Db      20932 GACTGTCCATACACTCCGTTGACTTCATCCGCTCGACCTCGATGCTAGACACCACT 20991

Qy      241 AAG 243
Db      20992 AAG 20994

RESULT 7
AX090361      44 bp      DNA      linear      PAT 21-MAR-2001
LOCUS
DEFINITION   Sequence 54 from Patent WO0116308.
ACCESSION   AX090361
VERSION      AX090361.1  GI:13444222
KEYWORDS

```

```

SOURCE          synthetic construct
ORGANISM        synthetic construct
REFERENCE
1
AUTHORS        Laessner,M. and van Eenennaam,A.
TITLE          Plant sterol acyltransferases
JOURNAL        Patent: WO 0116308-A 54 08-MAR-2001;
MONSANTO COMPANY (US)
FEATURES
source
1..44
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide primer"

ORIGIN
Query Match          1.6%; Score 27; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGGAGCGCAATTCGAATCAGTAACG 27
Db      18  ATGGAGCGCAATTCGAATCAGTAACG 44

RESULT 8
AX090362/c     40 bp      DNA      linear      PAT 21-MAR-2001
LOCUS
DEFINITION   Sequence 55 from Patent WO0116308.
ACCESSION   AX090362
VERSION      AX090362.1  GI:13444223
KEYWORDS
ORGANISM        synthetic construct
SOURCE          synthetic construct
REFERENCE
1
AUTHORS        Laessner,M. and van Eenennaam,A.
TITLE          Plant sterol acyltransferases
JOURNAL        Patent: WO 0116308-A 55 08-MAR-2001;
MONSANTO COMPANY (US)
FEATURES
source
1..40
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide primer"

ORIGIN
Query Match          1.6%; Score 26; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1616 GGGAGCTTGATTAAGTGGTATTAA 1641
Db      40  GGGAGCTTGATTAAGTGGTATTAA 15

RESULT 9
AF493159      2609 bp      mRNA      linear      PLN 02-DEC-2002
LOCUS
DEFINITION   Medicago truncatula putative phosphatidylcholine acyltransferase
ACCESSION   AF493159
VERSION      AF493159.1  GI:25992000
KEYWORDS
SOURCE          Medicago truncatula (barrel medic)
ORGANISM        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 2609)
Benveniste,P., Bouvier-Nave,P., Schaller,H. and Noiriell,A.

```


TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Acyltransferases involved in lipid (sterol) biosynthesis
Unpublished
2 (bases 1 to 2609)
Benveniste, P., Bouvier-Nave, P., Schaller, H. and Notriiel, A.
Direct Submission
Submitted (15-MAR-2002) Plant Molecular Biology Institute, CNRS, 28
rue Goethe, Strasbourg 67083, France
Location/Qualifiers
1. 2609
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone_11b="Samuel Roberts Noble Foundation Medicago
truncatula insect herbivory library (Korth, K., et al.,
unpublished)"
/note="fabaceae; sequence derived from EST clones BE321377
and B1267156"
82. 1980
/note="enzyme involved in the metabolism of phospholipids
and sterols"
/codon_start=1
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/protein_id="AA077002.1"
/db_xref="GI:25992001"
/translation="MANKPFLIFSLFLAVAGSGSGSELDYSKLSGIIIGFAS
TOLRAMSILDCPSPLDENPDLVLDITKLSAVNCMLKMLDPYQTHPOCKSR
PDGSLSGITELDPGILGTLSSVWKEWIKCIBGIBENANIIIVAPYDMRLSPMLEER
DLVPHKULITRETAFLKLGSPSLVNGSLGNNVRYFLFEMKLEIAPHYIQLNDQHT
HAFVAVAPLQATETITATISGTFGLPVEGTRMLFNSFASLWMPFSKTCRAS
NKYWGFGSGQVGTNTYCHDEBFKNSGMPKTIINIEIPIRGFFAYSPSEIPE
ANLSGMECGLPTOLSFSAEITADGSPFAIDYDPDSKRLIYOLEKSLAGDPVNPPLT
PMDRPIKNVFCIYGSNSKTKYGFAPSGPYDPNWIITIVVEYEGSLVTRSGNLY
VGNPGISGDETPYNSLSCKNMWLGSPVNTITRAPQSHDSDPOIDLVNHHGDDI
VPNTRFPRVATKITYIBSESLPKRKTAVWELDRANHNITRASSLWMLBEMWRDI
HPDASEFVTRAKRGPLRDEDCYMWYGARCAWPEYCEIRYVFGVHLGSGCRLYTS
ADLLHYL"

ORIGIN

Query Match 1.5%; Score 25; DB 8; Length 2609;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 627 GCTAGAAATGCACCAAAACATTAT 651
|||||
687 GCTAGAAATGCACCAAAACATTAT 711

Db

RESULT 10
TRBVSGAAB 2638 bp DNA linear INV 26-APR-1993
LOCUS
DEFINITION T.brucei variant surface glycoprotein (VSG) basic copy (BC) DNA, 5'
non-coding region.
ACCESSION M16036
VERSION M16036.1 GI:162431
KEYWORDS antigen; basic-copy gene; glycoprotein; variant surface antigen;
variant surface glycoprotein.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 2638)
AUTHORS Lee, M.G. and Van der Ploeg, L.H.
TITLE VSG gene
JOURNAL Mol. Cell. Biol. 7 (1), 357-364 (1987)
MEDLINE 87172726
PUBMED 3031467
COMMENT Original source text: T.brucei (variant 118) DNA, clone 1.
FEATURES
source location/Qualifiers
1. 2638
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/db_xref="taxon:5691"

ORIGIN

Query Match 1.3%; Score 21; DB 3; Length 2638;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1259 CCCCAAGTGGCAACCTTATC 1279
|||||
Db 239 CCCCAAGTGGCAACCTTATC 259

RESULT 11
AC073993/c 38785 bp DNA linear PRI 09-JAN-2002
LOCUS
DEFINITION Homo sapiens BAC clone RP11-674L1 from 2, complete sequence.
AC073993
AC073993.4 GI:15431257
VERSION
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 38785)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 38785)
AUTHORS Grewal, N. and Hakkenon, W.
TITLE The sequence of Homo sapiens BAC clone RP11-674L1
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 38785)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 38785)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (05-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 38785)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 5, 2001 this sequence version replaced gi:15187296.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUOSG
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0674L01

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPc1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P. Y., Zhao, B., Frengen, E., Tateo, M., Cacanese, J. V. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-318K6, 2000 bp overlap; the clone sequenced to the right is RP11-70L16, 2000 bp overlap.

Actual start of this clone is at base position 127793 of RP11-318K6; actual end is at base position 73456 of RP11-70L16.

Location/Qualifiers

1. 38785

FEATURES

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone="RP11-674L1"
/clone.lib="RPc1-11"
268..567
/rpc_family="Alu"
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2001..2022
/rpc_family="AT_rich"
repeat_region
2012..2491
/rpc_family="L1"
repeat_region
2492..3130
/rpc_family="L1"
repeat_region
3134..4785
/rpc_family="L1"
repeat_region
4018..4040
/rpc_family="(A)n"
repeat_region
4434..4467
/rpc_family="(TTTA)n"
repeat_region
4834..5194
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repeat_region
5203..5726
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repeat_region
5858..5911
/rpc_family="L1"
repeat_region
5912..6199
/rpc_family="Alu"
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6193..6234
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6200..7682
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7694..7752
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7753..8630
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8631..8888
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8891..9599
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repeat_region
9600..9800
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repeat_region
9801..9917
/rpc_family="L1"
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9803..9891
/rpc_family="L1"
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/note="match to EST AA435786 (NID:92140700) zc77e09.s1"
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10539..10613
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repeat_region 11710..12008
/rpc_family="Alu"
repeat_region 11872..11898
/rpc_family="AT_rich"
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/rpc_family="AT_rich"
repeat_region 12239..12292
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repeat_region 12390..12435
/rpc_family="AT_rich"
repeat_region 13069..13380
/rpc_family="Alu"
repeat_region 13074..13096
/rpc_family="(TTTA)n"
repeat_region 13951..14051
/rpc_family="MIR"
repeat_region 14347..14913
/rpc_family="L1"
repeat_region 14605..14642
/rpc_family="AT_rich"
repeat_region 14967..15230
/rpc_family="L2"
repeat_region 15310..15436
/rpc_family="MIR"
repeat_region 15814..16114
/rpc_family="Alu"
repeat_region 15929..15952
/rpc_family="AT_rich"
repeat_region 15957..16257
/note="match to EST AA435786 (NID:92140700) zc77e09.s1"
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/rpc_family="L2"
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/rpc_family="MER2_type"
repeat_region 17778..18022
/note="match to EST Z21373 (NID:928116)"
repeat_region 17838..17915
/rpc_family="(TATG)n"
repeat_region 18345..18390
/rpc_family="ERVU"
repeat_region 19325..19452
/rpc_family="L1"
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/rpc_family="L1"
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/rpc_family="Alu"
repeat_region 21120..21141
/rpc_family="AT_rich"
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/rpc_family="ERVU"
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/rpc_family="AT_rich"
repeat_region 23021..23573
/rpc_family="L1"
repeat_region 23574..24284
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repeat_region 25737..25787
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Query Match 1.3%; Score 21; DB 9; Length 38785;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 509 ACTTCACAGCTCAAGTTGA 529

```

Db      28342 ACTTCACAGCTCAAGTTGA 28322

RESULT 12
LOCUS   AL929207/c
DEFINITION
Zebrafish DNA sequence from clone CH211-214P16 in linkage group 17
Contains a novel gene for a protein similar to human mitochondrial
isoleucine tRNA synthetase, a novel gene similar to RAB3GAP (RAB3
GTPase-activating protein), a novel gene similar to PEP1CB (protein
phosphatase 1, catalytic subunit, beta isoform), two novel genes
and a CpG island, complete sequence.
ACCESSION
AL929207
VERSION
AL929207.5 GI:25252137
KEYWORDS
HTG; CpG island; GTPase-activating; isoleucine tRNA synthetase;
PEP1CB; protein phosphatase; RAB3; RAB3GAP.
SOURCE
Danio rerio (zebrafish)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 70206)
Babbage,A.
Direct Submission
Submitted (20-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zf1sh-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Nov 24, 2002 this sequence version replaced gi:25168772.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em1, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
from a CHORI-211 BAC library
VECTOR: pTARBAC2.1
IMPORTANT: This sequence is not the entire insert of clone
CH211-214P16 it may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone CH211-214P16 is at 1 in this sequence.
The true left end of clone DKEX-98G12 is at 68207 in this sequence.
Clone-derived Zebrafish pUC subclones occasionally display
inconsistency over the length of mononucleotide A/T runs and
conserved TA repeats. Where this is found the longest good quality
representation will be submitted.
Repeat names beginning 'Dr' were identified by the Recon repeat
discovery system (Zhurong Bao and Sean Eddy, submitted), and those
beginning 'drr' were identified by Rick Waterman (Stephen Johnson
lab, WashU). For further information see
http://www.sanger.ac.uk/projects/D_rerio/fishmask.shtml
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zf1sh-help@sanger.ac.uk
-----
Location/Qualifiers
1..70206
/organism="Danio rerio"

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repeat_region
/note="Dr000004 repeat: matches 1..442 of consensus"
850..1045
/note="Dr000012 repeat: matches 211..415 of consensus"
complement(1148..1352)
repeat_region
/note="TDR16 repeat: matches 41..254 of consensus"
1526..1537
/note="2.0 copies 6 mer GCCTTT 24% conserved"
1542..1561
/note="5.0 copies 4 mer AGAC 22% conserved"
1544..1566
/note="2.6 copies 9 mer ACGAAGA 30% conserved"
2246..2256
/note="3.7 copies 3 mer TTA 22% conserved"
2291..2318
/note="2.3 copies 12 mer ATTGTATATTA 47% conserved"
2300..2318
/note="3.2 copies 6 mer TTATT 22% conserved"
2320..2519
/note="Dr000276 repeat: matches 1..198 of consensus"
2520..2687
/note="TDR7 repeat: matches 2..463 of consensus"
complement(2689..2787)
/note="ACOBAT1 repeat: matches 779..865 of consensus"
2714..2800
/note="ACOBAT1 repeat: matches 779..865 of consensus"
2871..2903
/note="3.0 copies 11 mer ATTTATTTT 39% conserved"
2879..2893
/note="3.8 copies 4 mer TTTA 23% conserved"
3017..3026
/note="2.0 copies 5 mer TAATT 20% conserved"
3414..3427
/note="2.0 copies 7 mer GTTTGCG 28% conserved"
3805..3908
/note="Dr000349 repeat: matches 5..108 of consensus"
3909..3924
/note="16.0 copies 1 mer T 32% conserved"
4149..4163
/note="5.0 copies 3 mer TAT 23% conserved"
4285..4301
/note="2.8 copies 6 mer TTATG 27% conserved"
complement(4889..6150)
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/complement(join(4889..5336,6065..6150))
/gene="SI:zC214P16.1"
/product="SI:zC214P16.1 (novel protein)"
/note="match: ESTs: Em:BI842764 Em:AL927523 Em:BM081467
Em:BI472229"
/evidence="not_experimental"
5000..5012
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complement(join(5175..5336,6065..6136))
/gene="SI:zC214P16.1"
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/evidence="not_experimental"
/product="SI:zC214P16.1 (novel protein)"
/protein_id="CAD61266.1"
/db_xref="GI:27884147"
/translation="MKRQQLITLCGLMLLTLPSTSDKSGADSGKPSQPTNNNT
NTNTAGATDAAGLDVLPMTCLLPATLSPFH"
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/note="2.8 copies 5 mer TTTTG 28% conserved"
5514..5546
/note="3.3 copies 10 mer TTAAGTTAT 48% conserved"
5618..5891
/note="ANGEL repeat: matches 13..312 of consensus"
6017..6028
/note="12.0 copies 1 mer A 24% conserved"

```

FEATURES

SOURCE

LOCUS	AL603869	74349 bp	DNA	linear	PRI 27-SEP-2001
Repeat_region	complement (6575..6665)				
Repeat_region	/note="ANGEL repeat: matches 213..315 of consensus"				
Repeat_region	complement (6663..6730)				
Repeat_region	/note="Dr000403 repeat: matches 3..71 of consensus"				
Repeat_region	6724..6907				
Repeat_region	/note="ANGEL repeat: matches 93..290 of consensus"				
Repeat_region	7200..7215				
Repeat_region	/note="3.2 copies 5 mer GCTGT 32% conserved"				
Repeat_region	7237..7246				
Repeat_region	/note="2.5 copies 4 mer TCTG 20% conserved"				
Repeat_region	complement (7273..7742)				
Repeat_region	/gene="SI:zC214P16.2"				
Repeat_region	complement (join(7273..7442,7637..7742))				
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Repeat_region	/product="SI:zC214P16.2 (novel protein)"				
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Repeat_region	/product="SI:zC214P16.2 (novel protein)"				
Repeat_region	/protein_id="CAD61267.1"				
Repeat_region	/db_xref="GI:27884148"				
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Repeat_region	/note="2.2 copies 5 mer ATAA 22% conserved"				
Repeat_region	7537..7554				
Repeat_region	/note="2.0 copies 9 mer TAAATATG 36% conserved"				
Repeat_region	7709..7719				
Repeat_region	/note="2.2 copies 5 mer TGTGT 22% conserved"				
Repeat_region	8395..8405				
Repeat_region	/note="11.0 copies 1 mer T 22% conserved"				
Repeat_region	complement (8440..9186)				
Repeat_region	/note="Dr000011 repeat: matches 247..1027 of consensus"				
Repeat_region	complement (9184..9319)				
Repeat_region	/note="Dr000068 repeat: matches 1..139 of consensus"				
Repeat_region	9499..9512				
Repeat_region	/note="4.7 copies 3 mer GGA 28% conserved"				
Repeat_region	9569..95705				
Repeat_region	/gene="SI:zC214P16.3"				
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Repeat_region	join(<9569..9748,10757..10879,11056..11209,12314..12462 12879..12928,13026..13135,13238..13325,13691..13806, 13879..14048,14732..14822,14976..15067,16099..16259, 16353..16455,19448..19541,19673..19781,19865..19967, 20256..20381,21436..21567,21984..22090,22165..22310, 22388..22578,24849..24993,25433..25705)				
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Repeat_region	/evidence=not experimental				
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Repeat_region	/evidence=not experimental				
Repeat_region	join(<9569..9748,10757..10879,11056..11209,12314..12462 12879..12928,13026..13135,13238..13325,13691..13806, 13879..14048,14732..14822,14976..15067,16099..16259, 16353..16455,19448..19541,19673..19781,19865..19967, 20256..20381,21436..21567,21984..22090,22165..22310, 22388..22578,24849..24993,25433..25705)				

DEFINITION	Human DNA sequence from clone RP11-202P3 on chromosome 13, complete sequence.
ACCESSION	AL603869
VERSION	AL603869.5 GI:15808267
KEYWORDS	HTG.
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 74349)
TITLE	Bates,K.
JOURNAL	Direct Submission
COMMENT	Submitted (27-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk <p>Requests: clonequerry@sanger.ac.uk</p> <p>On Sep 28, 2001 this sequence version replaced gi:15617331.</p> <p>During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences without a small overlap as described above.</p> <p>This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep</p> <p>This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13</p> <p>RP11-202P3 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm</p> <p>VECTOR: PBAC3.6</p> <p>IMPORTANT: This sequence is not the entire insert of clone RP11-202P3 it may be shorter because we sequence overlapping sections only once, except for a short overlap.</p> <p>The true right end of clone RP11-202P3 is at 74349 in this sequence. The true right end of clone RP11-272M24 is at 2000 in this sequence.</p> <p>Location/Qualifiers</p> <pre> 1..74349 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="13" /clone="RP11-202P3" /clone_id="RPCI-11.1" </pre>
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Best Local Similarity	100.0%; Prod. No. 8.2;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	20955 CTATATAAAATGATTTTGC 21015
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LOCUS	Locus comitriculatus var. japonicus genomic DNA, chromosome 6,
DEFINITION	clone:UJ706108, TM0082b, complete sequence.
ACCESSION	AP006356

VERSION AP006356.1 GI:31580987
 KEYWORDS HTG.
 SOURCE Lotus corniculatus var. japonicus (Lotus japonicus)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroside 1; Fabales; Fabaceae; Papilionoideae; Lotese; Lotus.

REFERENCE 1
 AUTHORS Asamiya, E., Kato, T., Sato, S., Nakamura, Y., Kaneko, T. and Tabata, S.
 TITLE Structural Analysis of a Lotus japonicus Genome. IV. Sequence Features and Mapping of seventy-three TAC clones which cover the 7.5 Mb Regions of the Genome
 JOURNAL DNA Res. (2003) In press
 REFERENCE 2 (bases 1 to 93398)
 AUTHORS Sato, S.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAY-2003) Shushei Sato, Kazusa DNA Research Institute, Department of Plant Gene Research, 2-6-7 Kazusa-Kamatairi, Kisarazu, Chiba 292-0818, Japan (E-mail: ssato@kazusa.or.jp, URL: http://www.kazusa.or.jp/, Tel: 81-438-52-3935 (ex.2337), Fax: 81-438-52-3934)
 FEATURES Location/Qualifiers
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 /organism="Lotus corniculatus var. japonicus"
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 /chromosome="6"
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 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1102 TATGACCCAGATGACAGAGG 1122
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 Db 29743 TATGACCCAGATGACAGAGG 29723

RESULT 15
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 LOCUS Homo sapiens BAC clone RP11-174114 from 7, complete sequence.
 DEFINITION AC006988
 AC006988.3 GI:9857575
 VERSION HTG.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 107430)
 AUTHORS Sulston, J.E. and Wilson, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074

REFERENCE 2 (bases 1 to 107430)
 AUTHORS Courtney, L., Merry, B. and Stoneking, T.
 TITLE The sequence of Homo sapiens BAC clone RP11-174114
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 107430)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (05-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 107430)
 AUTHORS Waterston, R.H.

TITLE Direct Submission
 JOURNAL Submitted (19-AUG-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 107430)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 6 (bases 1 to 107430)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (29-APR-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 REFERENCE 7 (bases 1 to 107430)
 AUTHORS Wilson, R.
 TITLE Direct Submission
 JOURNAL Submitted (08-OCT-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT On Aug 19, 2000 this sequence version replaced gi:6094669.

----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu
 Contact: sapiens@wustl.wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0174114

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 The sequence of this clone was established as part of a mapping and sequencing collaboration between the NCRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/CTB/CHR7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu>

SOURCE INFORMATION:
 The RCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tareno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.reagen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is CTA-326K9, 200 bp overlap the clone sequenced to the right is CTA-305H12, 200 bp overlap. Actual start of this clone is at base position 94662 of CTA-326K9 actual end is at base position 6707 of CTA-305H12.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 79487 TCAAGTGACCTTGAACCTG 79507
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Search completed: November 9, 2004, 06:44:54
Job time : 7115 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 9, 2004, 02:28:27 ; Search time 157 Seconds
(without alignments)
7429.328 Million cell updates/sec

Title: US-09-651-651-4
Perfect score: 1641
Sequence: 1 atgggagcgcgaatcgaatc.....ctgataaagctgggtatcaa 1641

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	1.2	4	US-09-248-796A-11388	Sequence 11388, A
2	2488	1.2	4	US-08-956-171E-107	Sequence 107, App
3	2488	1.2	4	US-08-781-986A-107	Sequence 107, App
4	125	1.1	4	US-09-513-999C-16375	Sequence 16375, A
5	153	1.1	4	US-09-513-999C-23083	Sequence 23083, A
6	186	1.1	3	US-09-134-001C-396	Sequence 396, App
7	241	1.1	4	US-09-389-681-371	Sequence 371, App
8	241	1.1	4	US-09-620-405B-371	Sequence 371, App
9	241	1.1	4	US-09-433-826B-371	Sequence 371, App
10	241	1.1	4	US-09-604-287A-371	Sequence 371, App
11	241	1.1	4	US-09-834-759-371	Sequence 371, App
12	241	1.1	4	US-09-590-751A-371	Sequence 371, App
13	451	1.1	4	US-09-643-597-325	Sequence 325, App
14	451	1.1	4	US-09-480-884A-325	Sequence 325, App
15	451	1.1	4	US-09-542-615A-325	Sequence 325, App
16	451	1.1	4	US-09-606-421B-325	Sequence 325, App
17	451	1.1	4	US-09-630-940B-325	Sequence 325, App
18	474	1.1	4	US-09-248-796A-13889	Sequence 13889, A
19	489	1.1	4	US-09-513-999C-57489	Sequence 57489, A
20	1232	1.1	4	US-09-620-312D-672	Sequence 672, App
21	3278	1.1	1	US-08-484-105-13	Sequence 13, Appl
22	3278	1.1	1	US-08-484-105-13	Sequence 13, Appl
23	5873	1.1	4	US-09-620-312D-530	Sequence 530, App
24	5873	1.1	4	US-09-620-312D-260	Sequence 260, App
25	4403765	3	3	US-09-103-840A-2	Sequence 2, Appl
26	4411529	3	3	US-09-103-840A-1	Sequence 1, Appl
27	149	1.0	4	US-09-513-999C-22228	Sequence 22228, A

28	17	1.0	191	4	US-09-513-999C-34106	Sequence 34106, A
29	17	1.0	274	4	US-09-313-294A-6239	Sequence 6239, Ap
30	17	1.0	321	4	US-09-134-000C-1233	Sequence 1233, Ap
31	17	1.0	346	3	US-08-651-155B-59	Sequence 59, Appl
32	17	1.0	346	4	US-09-194-036B-59	Sequence 59, Appl
33	17	1.0	543	4	US-09-248-796A-3823	Sequence 3823, Ap
34	17	1.0	754	4	US-09-016-434-43	Sequence 43, Appl
35	17	1.0	906	4	US-09-252-991A-15711	Sequence 15711, A
36	17	1.0	966	4	US-09-328-352-3501	Sequence 3501, Ap
37	17	1.0	1093	3	US-09-651-656-24	Sequence 24, Appl
38	17	1.0	1093	3	US-09-650-855-24	Sequence 24, Appl
39	17	1.0	1095	4	US-09-489-039A-1654	Sequence 1654, Ap
40	17	1.0	1122	4	US-09-328-352-3060	Sequence 3060, Ap
41	17	1.0	1251	4	US-09-107-532A-2988	Sequence 2988, Ap
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43	17	1.0	1548	4	US-09-252-991A-15680	Sequence 15680, A
44	17	1.0	1551	4	US-09-614-221A-531	Sequence 531, App
45	17	1.0	1750	3	US-09-345-882-28	Sequence 28, Appl
46	17	1.0	2200	2	US-08-626-685A-9	Sequence 9, Appl
47	17	1.0	2200	4	US-08-899-112B-9	Sequence 9, Appl
48	17	1.0	2200	4	US-09-011-553-3	Sequence 3, Appl
49	17	1.0	2748	4	US-09-583-110-439	Sequence 439, App
50	17	1.0	4214	4	US-09-221-017B-293	Sequence 293, App
51	17	1.0	4226	4	US-09-620-312D-480	Sequence 480, App
52	17	1.0	5474	3	US-09-040-738-1	Sequence 1, Appl
53	17	1.0	5474	3	US-08-652-426A-1	Sequence 1, Appl
54	17	1.0	6002	3	US-09-345-882-4	Sequence 4, Appl
55	17	1.0	7786	2	US-09-770-988-2	Sequence 2, Appl
56	17	1.0	35100	2	US-08-737-379-17	Sequence 17, Appl
57	17	1.0	35100	3	US-08-757-669A-17	Sequence 17, Appl
58	17	1.0	35100	3	US-09-230-371A-17	Sequence 17, Appl
59	17	1.0	162450	3	US-09-345-882-1	Sequence 1, Appl
60	17	1.0	162450	4	US-08-916-421B-1	Sequence 1, Appl
61	17	1.0	1664976	4	US-09-692-570-1	Sequence 1, Appl
62	16	1.0	23	1	US-08-378-081B-124	Sequence 124, App
63	16	1.0	23	1	US-08-379-081B-126	Sequence 126, App
64	16	1.0	23	1	US-08-379-078-124	Sequence 124, App
65	16	1.0	23	1	US-08-379-078-126	Sequence 126, App
66	16	1.0	140	4	US-09-702-705-1392	Sequence 1392, App
67	16	1.0	140	4	US-09-726-457-1392	Sequence 1392, App
68	16	1.0	140	4	US-09-614-148B-1392	Sequence 1392, App
69	16	1.0	140	4	US-09-671-335-1392	Sequence 1392, App
70	16	1.0	140	4	US-09-658-824-1392	Sequence 1392, App
71	16	1.0	148	4	US-09-513-999C-32003	Sequence 32003, A
72	16	1.0	186	4	US-09-248-796A-9469	Sequence 9469, App
73	16	1.0	189	3	US-09-003-198A-18	Sequence 18, Appl
74	16	1.0	195	4	US-09-248-796A-13240	Sequence 13240, A
75	16	1.0	199	4	US-09-896-056A-8	Sequence 8, Appl
76	16	1.0	200	3	US-08-766-355-5	Sequence 5, Appl
77	16	1.0	200	3	US-09-003-198A-5	Sequence 5, Appl
78	16	1.0	200	3	US-09-428-805-5	Sequence 5, Appl
79	16	1.0	210	4	US-09-513-999C-19498	Sequence 19498, A
80	16	1.0	229	4	US-09-513-999C-29912	Sequence 29912, A
81	16	1.0	234	4	US-09-134-000C-1942	Sequence 1942, Ap
82	16	1.0	246	4	US-09-513-999C-20559	Sequence 20559, A
83	16	1.0	250	3	US-08-766-355-13	Sequence 13, Appl
84	16	1.0	250	3	US-09-003-198A-13	Sequence 13, Appl
85	16	1.0	250	3	US-09-428-805-13	Sequence 13, Appl
86	16	1.0	252	2	US-08-630-822A-97	Sequence 97, Appl
87	16	1.0	252	2	US-09-005-069-97	Sequence 97, Appl
88	16	1.0	252	2	US-08-906-769-104	Sequence 104, App
89	16	1.0	252	3	US-08-906-616-104	Sequence 104, App
90	16	1.0	252	3	US-08-817-795-104	Sequence 104, App
91	16	1.0	252	3	US-08-639-075A-104	Sequence 104, App
92	16	1.0	252	3	US-09-012-431-104	Sequence 104, App
93	16	1.0	252	3	US-09-012-692-104	Sequence 104, App
94	16	1.0	252	3	US-08-906-613-104	Sequence 104, App
95	16	1.0	252	3	US-09-171-156A-46	Sequence 46, Appl
96	16	1.0	252	4	US-09-004-730A-46	Sequence 46, Appl
97	16	1.0	252	4	US-08-981-799A-46	Sequence 46, Appl
98	16	1.0	252	5	PCT-US95-14442A-104	Sequence 104, App
99	16	1.0	271	4	US-09-896-056A-5	Sequence 5, Appl
100	16	1.0	277	4	US-09-896-056A-7	Sequence 7, Appl

101	16	1.0	282	4	US-09-540-236-207	Sequence 207, App	174	16	1.0	720	4	US-09-270-767-35226	Sequence 2526, A
102	16	1.0	283	4	US-09-896-096A-10	Sequence 10, Appl	175	16	1.0	724	3	US-08-858-207A-206	Sequence 206, App
103	16	1.0	287	4	US-09-513-999C-29021	Sequence 29021, A	176	16	1.0	756	4	US-09-543-681A-2342	Sequence 2342, App
104	16	1.0	297	4	US-09-107-533A-88	Sequence 88, Appl	177	16	1.0	768	4	US-09-248-796A-5524	Sequence 5524, App
105	16	1.0	386	2	US-08-967-101-52	Sequence 52, Appl	178	16	1.0	784	4	US-10-101-464A-340	Sequence 340, App
106	16	1.0	386	2	US-08-592-541-52	Sequence 52, Appl	179	16	1.0	795	4	US-09-266-965-57	Sequence 57, Appl
107	16	1.0	386	2	US-09-124-698-52	Sequence 52, Appl	180	16	1.0	811	3	US-09-662-250A-15	Sequence 15, Appl
108	16	1.0	386	3	US-09-127-480-52	Sequence 52, Appl	181	16	1.0	813	3	US-08-906-769-128	Sequence 128, App
109	16	1.0	386	3	US-08-496-841C-52	Sequence 52, Appl	182	16	1.0	815	3	US-08-906-616-128	Sequence 128, App
110	16	1.0	386	3	US-09-124-523-52	Sequence 52, Appl	183	16	1.0	815	3	US-08-639-075A-128	Sequence 128, App
111	16	1.0	386	4	US-09-636-796A-52	Sequence 52, Appl	184	16	1.0	815	3	US-09-012-431-128	Sequence 128, App
112	16	1.0	386	4	US-08-431-048F-52	Sequence 52, Appl	185	16	1.0	815	3	US-09-012-692-128	Sequence 128, App
113	16	1.0	389	4	US-09-270-767-2342	Sequence 2342, App	186	16	1.0	815	3	US-08-906-613-128	Sequence 128, App
114	16	1.0	389	4	US-09-270-767-17624	Sequence 17624, A	187	16	1.0	871	4	US-09-270-767-4493	Sequence 2493, App
115	16	1.0	459	4	US-09-513-999C-13735	Sequence 13735, A	188	16	1.0	871	4	US-09-270-767-17775	Sequence 17775, A
116	16	1.0	459	3	US-09-286-529-7	Sequence 7, Appl1	189	16	1.0	903	3	US-09-134-001C-1925	Sequence 1925, App
117	16	1.0	469	2	US-08-967-101-63	Sequence 63, Appl	190	16	1.0	915	4	US-09-462-845-8	Sequence 8, Appl1
118	16	1.0	469	2	US-08-592-541-63	Sequence 63, Appl	191	16	1.0	925	3	US-08-714-918-59	Sequence 59, Appl
119	16	1.0	469	3	US-09-124-698-63	Sequence 63, Appl	192	16	1.0	925	3	US-09-265-315-59	Sequence 59, Appl
120	16	1.0	469	3	US-09-127-480-63	Sequence 63, Appl	193	16	1.0	925	3	US-09-265-315-59	Sequence 59, Appl
121	16	1.0	469	3	US-08-496-841C-63	Sequence 63, Appl	194	16	1.0	925	3	US-09-266-417-59	Sequence 59, Appl
122	16	1.0	469	3	US-09-124-523-63	Sequence 63, Appl	195	16	1.0	925	4	US-09-528-709-59	Sequence 59, Appl
123	16	1.0	469	4	US-09-636-796A-63	Sequence 63, Appl	196	16	1.0	925	4	US-09-527-745-59	Sequence 59, Appl
124	16	1.0	469	4	US-08-431-048F-63	Sequence 63, Appl	197	16	1.0	930	4	US-09-252-991A-11343	Sequence 11343, A
125	16	1.0	470	4	US-09-621-976-9030	Sequence 9030, App	198	16	1.0	945	2	US-08-967-101-6	Sequence 6, Appl1
126	16	1.0	480	4	US-09-404-879A-60	Sequence 60, Appl	199	16	1.0	945	2	US-08-967-101-160	Sequence 160, App
127	16	1.0	480	4	US-09-338-933-60	Sequence 60, Appl	200	16	1.0	945	2	US-08-592-541-6	Sequence 6, Appl1
128	16	1.0	480	4	US-09-215-681-60	Sequence 60, Appl	201	16	1.0	945	2	US-08-592-541-160	Sequence 160, App
129	16	1.0	480	4	US-09-216-003A-60	Sequence 60, Appl	202	16	1.0	945	3	US-08-888-077A-10	Sequence 10, Appl
130	16	1.0	480	4	US-09-667-857-60	Sequence 60, Appl	203	16	1.0	945	3	US-09-124-698-6	Sequence 6, Appl1
131	16	1.0	489	2	US-08-967-101-74	Sequence 74, Appl	204	16	1.0	945	3	US-09-124-698-160	Sequence 160, App
132	16	1.0	489	2	US-08-592-541-74	Sequence 74, Appl	205	16	1.0	945	3	US-09-127-480-6	Sequence 6, Appl1
133	16	1.0	489	3	US-09-124-698-74	Sequence 74, Appl	206	16	1.0	945	3	US-09-127-480-160	Sequence 160, App
134	16	1.0	489	3	US-09-127-480-74	Sequence 74, Appl	207	16	1.0	945	3	US-08-496-841C-6	Sequence 6, Appl1
135	16	1.0	489	3	US-08-496-841C-74	Sequence 74, Appl	208	16	1.0	945	3	US-08-496-841C-160	Sequence 160, App
136	16	1.0	489	3	US-09-124-523-74	Sequence 74, Appl	209	16	1.0	945	3	US-09-124-523-6	Sequence 6, Appl1
137	16	1.0	489	4	US-09-636-796A-74	Sequence 74, Appl	210	16	1.0	945	3	US-09-124-523-160	Sequence 160, App
138	16	1.0	489	4	US-08-431-048F-74	Sequence 74, Appl	211	16	1.0	945	4	US-09-636-796A-6	Sequence 6, Appl1
139	16	1.0	489	4	US-09-270-767-3331	Sequence 3331, App	212	16	1.0	945	4	US-09-636-796A-160	Sequence 160, App
140	16	1.0	489	4	US-09-270-767-18613	Sequence 18613, A	213	16	1.0	945	4	US-08-431-048F-6	Sequence 6, Appl1
141	16	1.0	490	3	US-09-003-198A-19	Sequence 19, Appl	214	16	1.0	984	4	US-09-489-039A-1913	Sequence 1913, App
142	16	1.0	491	4	US-09-896-096A-3	Sequence 3, Appl1	215	16	1.0	1029	3	US-09-107-532A-1842	Sequence 1842, App
143	16	1.0	498	2	US-08-967-101-62	Sequence 62, Appl	216	16	1.0	1038	3	US-09-004-838-128	Sequence 128, App
144	16	1.0	498	2	US-08-592-541-62	Sequence 62, Appl	217	16	1.0	1055	4	US-09-632-277A-1	Sequence 1, Appl1
145	16	1.0	498	3	US-09-124-698-62	Sequence 62, Appl	218	16	1.0	1071	4	US-09-270-767-1061	Sequence 1061, App
146	16	1.0	498	3	US-09-127-480-62	Sequence 62, Appl	219	16	1.0	1071	4	US-09-270-767-16343	Sequence 16343, A
147	16	1.0	498	3	US-08-496-841C-62	Sequence 62, Appl	220	16	1.0	1084	3	US-08-604-789B-14	Sequence 14, Appl
148	16	1.0	498	3	US-09-124-523-62	Sequence 62, Appl	221	16	1.0	1084	3	US-09-312-721A-14	Sequence 14, Appl
149	16	1.0	498	4	US-09-636-796A-62	Sequence 62, Appl	222	16	1.0	1084	4	US-09-733-300-14	Sequence 14, Appl
150	16	1.0	498	4	US-08-431-048F-62	Sequence 62, Appl	223	16	1.0	1086	3	US-09-134-001C-1208	Sequence 1208, App
151	16	1.0	507	3	US-08-766-355-10	Sequence 10, Appl	224	16	1.0	1114	4	US-09-896-096A-2	Sequence 2, Appl1
152	16	1.0	507	3	US-09-003-198A-10	Sequence 10, Appl	225	16	1.0	1122	4	US-09-248-796A-729	Sequence 729, App
153	16	1.0	507	3	US-09-428-805-10	Sequence 10, Appl	226	16	1.0	1137	4	US-09-543-681A-432	Sequence 432, App
154	16	1.0	531	4	US-09-404-879A-5	Sequence 5, Appl1	227	16	1.0	1164	2	US-08-794-796-1	Sequence 1, Appl1
155	16	1.0	531	4	US-09-338-933-5	Sequence 5, Appl1	228	16	1.0	1182	4	US-09-248-796A-4758	Sequence 4758, App
156	16	1.0	531	4	US-09-215-681-5	Sequence 5, Appl1	229	16	1.0	1232	4	US-09-799-451-665	Sequence 665, App
157	16	1.0	531	4	US-09-216-003A-5	Sequence 5, Appl1	230	16	1.0	1251	4	US-09-543-681A-848	Sequence 848, App
158	16	1.0	555	4	US-09-667-857-5	Sequence 5, Appl1	231	16	1.0	1251	4	US-09-543-681A-10014	Sequence 10014, A
159	16	1.0	555	4	US-09-270-767-8811	Sequence 8811, App	232	16	1.0	1302	4	US-09-252-991A-15634	Sequence 15634, A
160	16	1.0	555	4	US-09-270-767-24093	Sequence 24093, A	233	16	1.0	1347	3	US-09-286-529-18	Sequence 18, Appl
161	16	1.0	591	4	US-09-621-976-11719	Sequence 11719, A	234	16	1.0	1359	4	US-09-328-352-2036	Sequence 2036, App
162	16	1.0	591	4	US-09-710-279-3069	Sequence 3069, App	235	16	1.0	1377	4	US-09-252-991A-8614	Sequence 8614, App
163	16	1.0	603	4	US-09-248-796A-2041	Sequence 2041, App	236	16	1.0	1398	4	US-09-489-039A-264	Sequence 264, App
164	16	1.0	643	2	US-08-975-316-59	Sequence 59, Appl	237	16	1.0	1462	4	US-09-270-767-9923	Sequence 9923, App
165	16	1.0	643	4	US-09-615-192A-59	Sequence 59, Appl	238	16	1.0	1476	4	US-09-248-796A-1686	Sequence 1686, App
166	16	1.0	643	4	US-09-169-789-59	Sequence 59, Appl	239	16	1.0	1506	3	US-09-198-955A-13	Sequence 13, Appl
167	16	1.0	651	4	US-09-248-796A-2406	Sequence 2406, App	240	16	1.0	1506	3	US-09-694-531-13	Sequence 13, Appl
168	16	1.0	681	4	US-09-248-796A-2079	Sequence 2079, App	241	16	1.0	1506	4	US-10-072-152-13	Sequence 13, Appl
169	16	1.0	687	4	US-09-710-279-2935	Sequence 2935, App	242	16	1.0	1524	4	US-09-248-796A-4180	Sequence 4180, App
170	16	1.0	687	4	US-09-710-279-2935	Sequence 2935, App	243	16	1.0	1569	4	US-09-149-476-150	Sequence 150, App
171	16	1.0	699	3	US-09-276-531-91	Sequence 91, Appl	244	16	1.0	1629	4	US-09-248-796A-2029	Sequence 2029, App
172	16	1.0	711	3	US-09-134-001C-806	Sequence 806, App	245	16	1.0	1659	4	US-09-252-991A-15717	Sequence 15717, A
173	16	1.0	711	3	US-08-823-120-5	Sequence 5, Appl1	246	16	1.0	1722	4	US-09-328-352-2294	Sequence 2294, App

C 247	16	1.0	1760	4	US-09-270-767-1590	Sequence 1590, App	C 320	16	1.0	6422	4	US-09-976-594-715	Sequence 715, App
C 248	16	1.0	1760	4	US-09-270-767-16872	Sequence 16872, A	C 321	16	1.0	6593	4	US-08-961-527-195	Sequence 195, App
C 249	16	1.0	1840	4	US-09-620-312D-120	Sequence 120, App	C 322	16	1.0	6797	4	US-09-023-655-1087	Sequence 1087, App
C 250	16	1.0	1859	3	US-09-286-528-19	Sequence 19, App	C 323	16	1.0	6876	4	US-09-809-665A-15	Sequence 15, App
C 251	16	1.0	1921	2	US-08-557-128-11	Sequence 11, App	C 324	16	1.0	7152	3	US-09-167-681-29	Sequence 29, App
C 252	16	1.0	1921	2	US-08-557-128-11	Sequence 11, App	C 325	16	1.0	7445	3	US-09-178-973B-8	Sequence 8, App
C 253	16	1.0	1964	4	US-09-799-451-39	Sequence 39, App	C 326	16	1.0	7445	3	US-09-419-568F-8	Sequence 8, App
C 254	16	1.0	1971	4	US-10-140-002-139	Sequence 139, App	C 327	16	1.0	7445	3	US-09-354-243B-8	Sequence 8, App
C 255	16	1.0	2017	4	US-09-404-879A-72	Sequence 72, App	C 328	16	1.0	8224	2	US-09-010-1398-14	Sequence 14, App
C 256	16	1.0	2017	4	US-09-338-933-72	Sequence 72, App	C 329	16	1.0	8224	2	US-09-366-260-14	Sequence 14, App
C 257	16	1.0	2017	4	US-09-215-681-72	Sequence 72, App	C 330	16	1.0	8722	4	US-09-221-017B-263	Sequence 263, App
C 258	16	1.0	2017	4	US-09-216-003A-72	Sequence 72, App	C 331	16	1.0	9997	1	US-08-246-982A-15	Sequence 15, App
C 259	16	1.0	2022	4	US-09-667-857-72	Sequence 72, App	C 332	16	1.0	9997	1	US-08-246-982A-15	Sequence 15, App
C 260	16	1.0	2118	4	US-09-583-110-199	Sequence 199, App	C 333	16	1.0	10103	2	US-08-457-273B-7	Sequence 7, App
C 261	16	1.0	2118	4	US-09-800-729-34	Sequence 34, App	C 334	16	1.0	10103	2	US-08-457-273B-7	Sequence 7, App
C 262	16	1.0	2124	4	US-09-248-796A-1684	Sequence 3684, App	C 335	16	1.0	10348	3	US-08-556-419-13	Sequence 13, App
C 263	16	1.0	2133	4	US-09-661-322A-41	Sequence 41, App	C 336	16	1.0	10348	3	US-08-556-419-13	Sequence 13, App
C 264	16	1.0	2180	2	US-09-003-217-1	Sequence 1, App	C 337	16	1.0	10348	3	US-08-556-419-13	Sequence 13, App
C 265	16	1.0	2180	2	US-09-218-942-1	Sequence 1, App	C 338	16	1.0	10366	1	US-08-246-982A-5	Sequence 5, App
C 266	16	1.0	2189	4	US-09-106-568E-7	Sequence 7, App	C 339	16	1.0	10366	1	US-08-453-265-5	Sequence 5, App
C 267	16	1.0	2271	4	US-09-248-796A-3650	Sequence 3650, App	C 340	16	1.0	10862	3	US-09-058-411-1	Sequence 11, App
C 268	16	1.0	2375	4	US-08-956-171E-147	Sequence 147, App	C 341	16	1.0	10862	3	US-09-705-949-1	Sequence 1, App
C 269	16	1.0	2375	4	US-08-956-171E-147	Sequence 147, App	C 342	16	1.0	10892	4	US-09-452-638-52	Sequence 52, App
C 270	16	1.0	2358	4	US-08-781-986A-147	Sequence 147, App	C 343	16	1.0	10892	4	US-09-452-638-52	Sequence 52, App
C 271	16	1.0	2543	3	US-09-307-143-5	Sequence 5, App	C 344	16	1.0	11327	1	US-07-906-871-15	Sequence 15, App
C 272	16	1.0	2600	4	US-09-589-892B-1	Sequence 1, App	C 345	16	1.0	12084	4	US-09-526-193A-21	Sequence 21, App
C 273	16	1.0	2873	4	US-08-630-915A-193	Sequence 193, App	C 346	16	1.0	28001	4	US-09-819-993-3	Sequence 3, App
C 274	16	1.0	2905	3	US-09-468-578-3	Sequence 3, App	C 347	16	1.0	28001	4	US-10-193-285-3	Sequence 3, App
C 275	16	1.0	2905	3	US-09-468-578-3	Sequence 3, App	C 348	16	1.0	30549	3	US-09-134-001C-322	Sequence 322, App
C 276	16	1.0	2905	3	US-09-468-578-3	Sequence 3, App	C 349	16	1.0	30549	3	US-09-596-002-20	Sequence 20, App
C 277	16	1.0	2965	2	US-08-460-570-1	Sequence 1, App	C 350	16	1.0	31063	4	US-09-596-002-20	Sequence 20, App
C 278	16	1.0	2965	2	US-08-460-570-1	Sequence 1, App	C 351	16	1.0	31880	3	US-09-453-067-3	Sequence 3, App
C 279	16	1.0	2965	2	US-08-286-870A-1	Sequence 1, App	C 352	16	1.0	32679	4	US-08-976-063B-1	Sequence 1, App
C 280	16	1.0	2965	2	US-08-286-870A-1	Sequence 1, App	C 353	16	1.0	32679	4	US-08-976-063B-1	Sequence 1, App
C 281	16	1.0	3147	2	US-07-952-853-23	Sequence 23, App	C 354	16	1.0	33100	5	US-08-306-681B-19	Sequence 19, App
C 282	16	1.0	3147	2	US-08-914-848-23	Sequence 23, App	C 355	16	1.0	33100	5	PCT-US93-06251-19	Sequence 19, App
C 283	16	1.0	3226	4	US-08-539-205A-5	Sequence 5, App	C 356	16	1.0	33982	4	US-09-820-924-3	Sequence 3, App
C 284	16	1.0	3233	4	US-09-392-163A-5	Sequence 5, App	C 357	16	1.0	33982	4	US-09-820-924-3	Sequence 3, App
C 285	16	1.0	3273	4	US-09-710-279-3586	Sequence 3586, App	C 358	16	1.0	40352	3	US-08-846-111D-15	Sequence 15, App
C 286	16	1.0	3288	1	US-08-208-008C-3	Sequence 907, App	C 359	16	1.0	40352	3	US-09-443-077-15	Sequence 15, App
C 287	16	1.0	3632	4	US-09-710-279-4278	Sequence 3, App	C 360	16	1.0	53550	4	US-09-266-965-76	Sequence 76, App
C 288	16	1.0	3633	4	US-09-710-279-4035	Sequence 4035, App	C 361	16	1.0	53550	4	US-10-327-189-42	Sequence 42, App
C 289	16	1.0	3722	4	US-10-164-595-9	Sequence 9, App	C 362	16	1.0	53550	4	US-09-967-669-10	Sequence 10, App
C 290	16	1.0	3767	4	US-09-710-279-4213	Sequence 4213, App	C 363	16	1.0	74962	4	US-09-685-853A-3	Sequence 3, App
C 291	16	1.0	3781	4	US-09-710-279-3993	Sequence 3993, App	C 364	16	1.0	106746	4	US-09-326-402C-12	Sequence 12, App
C 292	16	1.0	3805	4	US-09-710-279-3687	Sequence 3687, App	C 365	16	1.0	106746	4	US-09-326-402C-12	Sequence 12, App
C 293	16	1.0	3862	4	US-10-164-595-5	Sequence 5, App	C 366	16	1.0	111793	4	US-09-148-806-3	Sequence 3, App
C 294	16	1.0	3877	2	US-08-599-895-1	Sequence 1, App	C 367	16	1.0	111793	4	US-09-822-871-3	Sequence 3, App
C 295	16	1.0	3877	2	US-08-599-895-1	Sequence 1, App	C 368	16	1.0	123025	4	US-10-027-983-11	Sequence 11, App
C 296	16	1.0	3877	3	US-09-211-290-1	Sequence 1, App	C 369	16	1.0	123025	4	US-09-211-290-1	Sequence 1, App
C 297	16	1.0	3877	3	US-09-322-676-1	Sequence 1, App	C 370	16	1.0	123025	4	US-09-211-290-1	Sequence 1, App
C 298	16	1.0	3937	4	US-10-164-595-7	Sequence 7, App	C 371	16	1.0	123025	4	US-09-211-290-1	Sequence 1, App
C 299	16	1.0	3985	4	US-10-164-595-3	Sequence 3, App	C 372	16	1.0	123025	4	US-09-211-290-1	Sequence 1, App
C 300	16	1.0	4176	4	US-09-106-568E-1	Sequence 1, App	C 373	16	1.0	123025	4	US-09-211-290-1	Sequence 1, App
C 301	16	1.0	4255	4	US-09-698-286A-8	Sequence 8, App	C 374	16	1.0	1644976	4	US-08-916-421B-1	Sequence 1, App
C 302	16	1.0	4269	4	US-09-540-236-1101	Sequence 1101, App	C 375	16	1.0	1644976	4	US-09-692-570-1	Sequence 1, App
C 303	16	1.0	4391	3	US-09-207-857-1	Sequence 1, App	C 376	16	1.0	1830121	4	US-09-557-884-1	Sequence 1, App
C 304	16	1.0	4391	3	US-09-207-857-1	Sequence 1, App	C 377	16	1.0	1830121	4	US-09-557-884-1	Sequence 1, App
C 305	16	1.0	4528	4	US-08-809-254A-6	Sequence 6, App	C 378	16	1.0	1830121	4	US-10-329-860-1	Sequence 1, App
C 306	16	1.0	4890	4	US-09-799-451-714	Sequence 714, App	C 379	16	1.0	4431529	3	US-09-103-840A-2	Sequence 2, App
C 307	16	1.0	4920	4	US-08-956-171E-26	Sequence 26, App	C 380	16	1.0	4431529	3	US-09-103-840A-2	Sequence 2, App
C 308	16	1.0	4920	4	US-08-781-986A-26	Sequence 26, App	C 381	15	0.9	18	4	US-09-422-978-4783	Sequence 4783, App
C 309	16	1.0	4931	4	US-09-809-665A-102	Sequence 102, App	C 382	15	0.9	30	3	US-09-180-100-6	Sequence 6, App
C 310	16	1.0	5009	4	US-09-106-568E-5	Sequence 5, App	C 383	15	0.9	33	3	US-08-454-928-3	Sequence 3, App
C 311	16	1.0	5078	4	US-09-620-312D-565	Sequence 565, App	C 384	15	0.9	49	4	US-09-104-067-1	Sequence 1, App
C 312	16	1.0	5171	4	US-08-956-171E-264	Sequence 264, App	C 385	15	0.9	51	4	US-09-443-199C-501	Sequence 501, App
C 313	16	1.0	5304	4	US-08-781-986A-264	Sequence 264, App	C 386	15	0.9	52	4	US-09-104-067-1	Sequence 1, App
C 314	16	1.0	5304	4	US-08-781-986A-264	Sequence 264, App	C 387	15	0.9	57	4	US-09-168-947-32	Sequence 32, App
C 315	16	1.0	5672	4	US-09-023-655-1392	Sequence 1392, App	C 388	15	0.9	73	4	US-09-513-999C-15343	Sequence 15343, App
C 316	16	1.0	5935	3	US-09-178-973B-17	Sequence 17, App	C 389	15	0.9	82	3	US-09-168-947-14	Sequence 14, App
C 317	16	1.0	5935	3	US-09-419-568F-29	Sequence 29, App	C 390	15	0.9	85	3	US-09-418-828A-10	Sequence 10, App
C 318	16	1.0	5935	3	US-09-354-243B-29	Sequence 29, App	C 391	15	0.9	126	1	US-08-480-884-9	Sequence 9, App
C 319	16	1.0	6415	4	US-08-961-527-162	Sequence 162, App	C 392	15	0.9	126	5	PCT-US94-08024-392	Sequence 9, App

333	15	0.9	160	4	US-09-513-999C-12383	Sequence 12383, A	C 466	15	0.9	483	1	US-08-644-664B-8	Sequence 8, Appl1
334	15	0.9	174	4	US-09-513-999C-11796	Sequence 11796, A	C 467	15	0.9	483	2	US-08-761-277A-8	Sequence 15, Appl1
C 335	15	0.9	186	4	US-09-248-796A-13139	Sequence 13139, A	C 468	15	0.9	483	2	US-08-715-808-15	Sequence 15, Appl1
C 336	15	0.9	192	4	US-09-107-532A-2041	Sequence 2041, Ap	C 469	15	0.9	483	4	US-09-621-976-17558	Sequence 17558, A
337	15	0.9	195	4	US-09-270-767-26579	Sequence 26579, A	C 470	15	0.9	483	4	US-09-270-767-12964	Sequence 12964, A
338	15	0.9	195	4	US-09-248-796A-9211	Sequence 9211, Ap	C 471	15	0.9	501	4	US-09-543-681A-1552	Sequence 1552, Ap
C 339	15	0.9	207	4	US-09-583-110-360	Sequence 360, App	C 472	15	0.9	501	4	US-09-248-796A-2357	Sequence 2357, Ap
C 400	15	0.9	207	4	US-09-513-999C-16168	Sequence 16168, A	C 473	15	0.9	501	4	US-09-248-796A-2400	Sequence 2400, Ap
C 401	15	0.9	212	4	US-09-016-434-50	Sequence 50, Appl1	C 474	15	0.9	504	4	US-09-252-991A-4925	Sequence 4925, Ap
C 402	15	0.9	213	4	US-09-248-796A-1081	Sequence 8081, Ap	C 475	15	0.9	504	4	US-09-248-796A-1506	Sequence 1506, Ap
C 403	15	0.9	216	4	US-09-248-796A-11498	Sequence 11498, A	C 476	15	0.9	510	4	US-09-621-976-840	Sequence 840, App
C 404	15	0.9	222	4	US-09-248-796A-10858	Sequence 10858, A	C 477	15	0.9	514	4	US-09-621-976-145	Sequence 145, App
C 405	15	0.9	223	4	US-09-513-999C-18951	Sequence 18951, A	C 478	15	0.9	519	4	US-09-621-976-16272	Sequence 16272, A
C 406	15	0.9	234	4	US-09-248-796A-2960	Sequence 2960, Ap	C 479	15	0.9	525	4	US-09-248-796A-5156	Sequence 5156, Ap
C 407	15	0.9	246	4	US-09-583-110-359	Sequence 359, App	C 480	15	0.9	526	4	US-09-513-999C-13232	Sequence 13232, A
C 408	15	0.9	252	3	US-08-905-223-84	Sequence 84, Appl1	C 481	15	0.9	538	4	US-09-621-976-14167	Sequence 14167, A
C 409	15	0.9	253	4	US-09-513-999C-24560	Sequence 24560, A	C 482	15	0.9	540	1	US-07-990-965-1	Sequence 1, Appl1
C 410	15	0.9	258	4	US-09-248-796A-7591	Sequence 7591, Ap	C 483	15	0.9	540	4	US-09-252-991A-13817	Sequence 13817, A
C 411	15	0.9	261	4	US-09-248-796A-12391	Sequence 12391, A	C 484	15	0.9	540	4	US-09-270-767-8393	Sequence 8393, Ap
C 412	15	0.9	261	2	US-08-774-025A-2	Sequence 2, Appl1	C 485	15	0.9	540	4	US-09-270-767-23675	Sequence 23675, A
C 413	15	0.9	264	3	US-09-244-093-2	Sequence 2, Appl1	C 486	15	0.9	543	4	US-09-252-991A-1929	Sequence 1929, Ap
C 414	15	0.9	264	4	US-09-016-434-93	Sequence 93, Appl1	C 487	15	0.9	550	4	US-09-306-420C-17	Sequence 17, Appl1
C 415	15	0.9	264	4	US-09-619-758-2	Sequence 2, Appl1	C 488	15	0.9	550	4	US-09-306-420C-17	Sequence 19, Appl1
C 416	15	0.9	264	4	US-09-886-607-2	Sequence 2, Appl1	C 489	15	0.9	554	4	US-09-513-999C-1718	Sequence 1718, Ap
C 417	15	0.9	264	4	US-09-270-767-7357	Sequence 7357, Ap	C 490	15	0.9	556	4	US-09-621-976-1608	Sequence 1608, A
C 418	15	0.9	264	4	US-09-270-767-22639	Sequence 22639, A	C 491	15	0.9	558	4	US-09-252-991A-7770	Sequence 7770, Ap
C 419	15	0.9	267	4	US-09-107-532A-570	Sequence 570, App	C 492	15	0.9	562	4	US-09-513-999C-8342	Sequence 8342, Ap
C 420	15	0.9	276	4	US-09-023-665-82	Sequence 82, Appl1	C 493	15	0.9	568	3	US-08-998-416-1109	Sequence 1109, Ap
C 421	15	0.9	278	4	US-09-313-294A-6317	Sequence 6317, Ap	C 494	15	0.9	572	4	US-09-621-976-16094	Sequence 16094, A
C 422	15	0.9	278	4	US-09-313-294A-6427	Sequence 6427, Ap	C 495	15	0.9	572	4	US-09-270-767-7847	Sequence 7847, Ap
C 423	15	0.9	284	4	US-09-313-294A-3945	Sequence 3945, Ap	C 496	15	0.9	572	4	US-09-270-767-23129	Sequence 23129, A
C 424	15	0.9	287	4	US-09-313-294A-2011	Sequence 2011, Ap	C 497	15	0.9	574	1	US-08-612-890-1	Sequence 1, Appl1
C 425	15	0.9	291	4	US-09-489-039A-1696	Sequence 1696, Ap	C 498	15	0.9	583	6	5225348-8	Patent No. 5225348
C 426	15	0.9	291	4	US-09-134-000C-183	Sequence 183, App	C 499	15	0.9	583	4	US-09-270-391-24	Sequence 24, Appl1
C 427	15	0.9	299	4	US-09-248-796A-10407	Sequence 10407, A	C 500	15	0.9	585	3	US-08-075-520A-27	Sequence 27, Appl1
C 428	15	0.9	299	4	US-09-313-294A-6626	Sequence 6626, Ap	C 501	15	0.9	588	4	US-09-710-379-2119	Sequence 2119, Ap
C 429	15	0.9	312	4	US-09-489-039A-465	Sequence 465, App	C 502	15	0.9	589	4	US-09-621-976-17537	Sequence 17537, A
C 430	15	0.9	313	4	US-09-513-999C-24774	Sequence 24774, A	C 503	15	0.9	599	6	5225348-9	Patent No. 5225348
C 431	15	0.9	333	4	US-09-313-294A-3924	Sequence 3924, Ap	C 504	15	0.9	600	4	US-09-489-039A-4150	Sequence 4150, Ap
C 432	15	0.9	345	4	US-09-107-532A-1178	Sequence 1178, Ap	C 505	15	0.9	606	4	US-09-248-796A-4552	Sequence 4552, Ap
C 433	15	0.9	347	2	US-08-546-117-7	Sequence 7, Appl1	C 506	15	0.9	606	4	US-09-248-796A-4866	Sequence 4866, Ap
C 434	15	0.9	348	4	US-09-270-767-26920	Sequence 26920, A	C 507	15	0.9	612	4	US-09-248-796A-9210	Sequence 9210, Ap
C 435	15	0.9	353	4	US-09-513-999C-15687	Sequence 15687, A	C 508	15	0.9	613	4	US-09-497-855A-13	Sequence 13, Appl1
C 436	15	0.9	369	4	US-09-248-796A-8006	Sequence 8006, Ap	C 509	15	0.9	613	4	US-09-270-767-2331	Sequence 2331, Ap
C 437	15	0.9	374	4	US-09-513-999C-11764	Sequence 11764, A	C 510	15	0.9	613	4	US-09-270-767-5863	Sequence 5863, A
C 438	15	0.9	374	4	US-09-513-999C-17653	Sequence 17653, A	C 511	15	0.9	617	4	US-09-221-017B-321	Sequence 321, App
C 439	15	0.9	376	4	US-09-621-976-16394	Sequence 16394, A	C 512	15	0.9	618	3	US-09-385-982-59	Sequence 59, Appl1
C 440	15	0.9	384	4	US-09-107-532A-3130	Sequence 3130, Ap	C 513	15	0.9	618	4	US-09-543-681A-316	Sequence 316, App
C 441	15	0.9	387	4	US-09-270-767-28221	Sequence 28221, A	C 514	15	0.9	624	3	US-08-884-077-5	Sequence 5, Appl1
C 442	15	0.9	400	4	US-08-956-171E-848	Sequence 848, App	C 515	15	0.9	627	3	US-09-134-001C-2763	Sequence 2763, Ap
C 443	15	0.9	400	4	US-08-956-171E-3744	Sequence 3744, Ap	C 516	15	0.9	630	4	US-09-489-039A-1859	Sequence 1859, Ap
C 444	15	0.9	400	4	US-08-781-986A-848	Sequence 848, App	C 517	15	0.9	636	4	US-09-134-000C-2081	Sequence 2081, Ap
C 445	15	0.9	400	4	US-08-781-986A-3744	Sequence 3744, Ap	C 518	15	0.9	638	3	US-09-328-111-26	Sequence 26, Appl1
C 446	15	0.9	405	4	US-09-495-050A-213	Sequence 213, App	C 519	15	0.9	639	4	US-09-248-796A-1137	Sequence 1137, Ap
C 447	15	0.9	405	4	US-09-134-000C-744	Sequence 744, App	C 520	15	0.9	644	4	US-09-270-767-5869	Sequence 5869, Ap
C 448	15	0.9	406	4	US-09-621-976-16393	Sequence 16393, A	C 521	15	0.9	644	4	US-09-270-767-5863	Sequence 21151, A
C 449	15	0.9	408	4	US-09-248-796A-7532	Sequence 7532, Ap	C 522	15	0.9	645	4	US-09-543-681A-428	Sequence 428, App
C 450	15	0.9	409	4	US-09-513-999C-11382	Sequence 11382, A	C 523	15	0.9	651	4	US-09-328-352-350	Sequence 350, App
C 451	15	0.9	414	4	US-09-134-000C-2784	Sequence 2784, Ap	C 524	15	0.9	666	4	US-09-107-532A-3649	Sequence 3649, Ap
C 452	15	0.9	415	1	US-08-613-890-2	Sequence 2, Appl1	C 525	15	0.9	668	3	US-08-578-634C-2	Sequence 2, Appl1
C 453	15	0.9	416	4	US-09-497-493-22	Sequence 22, Appl1	C 526	15	0.9	668	3	US-09-430-010-2	Sequence 2, Appl1
C 454	15	0.9	417	4	US-09-513-999C-10080	Sequence 10080, A	C 527	15	0.9	669	3	US-08-928-941D-23	Sequence 23, Appl1
C 455	15	0.9	421	4	US-09-497-491-28	Sequence 28, Appl1	C 528	15	0.9	669	3	US-09-280-590A-23	Sequence 23, Appl1
C 456	15	0.9	432	4	US-09-621-976-2133	Sequence 2133, Ap	C 529	15	0.9	669	4	US-09-892-398-23	Sequence 23, Appl1
C 457	15	0.9	440	4	US-09-513-999C-12746	Sequence 12746, A	C 530	15	0.9	672	4	US-09-543-681A-1954	Sequence 1954, Ap
C 458	15	0.9	458	4	US-09-270-767-12454	Sequence 12454, A	C 531	15	0.9	673	4	US-09-270-767-7515	Sequence 7515, Ap
C 459	15	0.9	461	4	US-09-270-767-13991	Sequence 13991, Ap	C 532	15	0.9	673	4	US-09-270-767-22797	Sequence 22797, A
C 460	15	0.9	461	4	US-09-270-767-19273	Sequence 19273, A	C 533	15	0.9	681	4	US-09-471-573A-1	Sequence 1, Appl1
C 461	15	0.9	462	4	US-09-621-976-17620	Sequence 17620, A	C 534	15	0.9	702	4	US-09-328-352-2733	Sequence 2733, Ap
C 462	15	0.9	468	4	US-09-248-796A-10273	Sequence 10273, A	C 535	15	0.9	718	4	US-09-621-976-1814	Sequence 1814, Ap
C 463	15	0.9	474	4	US-09-446-880A-3	Sequence 3, Appl1	C 536	15	0.9	712	4	US-09-270-767-13229	Sequence 13229, A
C 464	15	0.9	478	4	US-09-621-976-1741	Sequence 1741, Ap	C 537	15	0.9	716	3	US-08-998-416-545	Sequence 545, App
C 465	15	0.9	480	4	US-09-543-681A-2611	Sequence 2611, Ap	C 538	15	0.9	717	4	US-09-107-532A-2548	Sequence 548, App

539	15	0.9	729	4	US-09-328-352-792	Sequence 792, App	612	15	0.9	948	4	US-09-599-360B-13	Sequence 11, Appl
540	15	0.9	732	4	US-09-601-198-112	Sequence 112, App	613	15	0.9	950	4	US-09-270-767-8142	Sequence 8142, App
541	15	0.9	735	4	US-09-328-352-3768	Sequence 3768, App	614	15	0.9	950	4	US-09-270-767-23424	Sequence 23424, App
542	15	0.9	747	4	US-09-583-110-1445	Sequence 1445, App	615	15	0.9	957	4	US-09-866-028-90	Sequence 90, Appl
543	15	0.9	753	3	US-09-134-001C-1562	Sequence 1562, App	616	15	0.9	957	4	US-09-944-457-90	Sequence 90, Appl
544	15	0.9	756	4	US-09-252-991A-2114	Sequence 2114, App	617	15	0.9	963	4	US-10-140-002-389	Sequence 389, App
545	15	0.9	759	4	US-09-134-000C-1071	Sequence 1071, App	618	15	0.9	978	4	US-09-134-000C-2710	Sequence 2710, App
546	15	0.9	759	4	US-09-248-796A-143	Sequence 143, App	619	15	0.9	984	4	US-09-248-796A-968	Sequence 968, App
547	15	0.9	762	4	US-09-124-796A-2906	Sequence 2906, App	620	15	0.9	987	1	US-08-186-529-1	Sequence 1, Appl1
548	15	0.9	780	4	US-09-134-000C-1237	Sequence 1237, App	621	15	0.9	987	3	US-08-640-386A-1	Sequence 1, Appl1
549	15	0.9	786	4	US-09-543-681A-3016	Sequence 3016, App	622	15	0.9	987	3	US-08-848-760B-24	Sequence 24, Appl
550	15	0.9	787	1	US-08-236-427-12	Sequence 12, Appl	623	15	0.9	987	4	US-09-489-039A-1978	Sequence 1978, App
551	15	0.9	791	3	US-08-858-207A-231	Sequence 231, App	624	15	0.9	987	4	US-09-826-025-24	Sequence 24, Appl
552	15	0.9	795	4	US-09-489-039A-1961	Sequence 1961, App	625	15	0.9	990	3	US-09-079-984A-11	Sequence 11, Appl1
553	15	0.9	798	2	US-08-319-866-7	Sequence 7, Appl1	626	15	0.9	990	3	US-09-079-984A-11	Sequence 11, Appl1
554	15	0.9	798	4	US-08-803-917-7	Sequence 7, Appl1	627	15	0.9	990	4	US-09-390-729-11	Sequence 11, Appl1
555	15	0.9	801	4	US-09-489-039A-646	Sequence 646, App	628	15	0.9	990	4	US-09-328-352-2754	Sequence 2754, App
556	15	0.9	803	3	US-08-454-928-9	Sequence 9, Appl1	629	15	0.9	993	4	US-09-328-352-2754	Sequence 2754, App
557	15	0.9	806	4	US-09-270-767-9377	Sequence 9377, App	630	15	0.9	999	4	US-09-489-039A-3748	Sequence 3748, App
558	15	0.9	806	4	US-09-270-767-24659	Sequence 24659, App	631	15	0.9	1008	4	US-09-583-110-1297	Sequence 1297, App
559	15	0.9	807	4	US-09-248-796A-3765	Sequence 3765, App	632	15	0.9	1008	4	US-09-270-767-13274	Sequence 13274, App
560	15	0.9	808	4	US-09-328-475C-109	Sequence 109, App	633	15	0.9	1017	4	US-08-184-009-194	Sequence 194, App
561	15	0.9	817	1	US-08-378-011A-4	Sequence 4, Appl1	634	15	0.9	1018	2	US-08-458-356-194	Sequence 194, App
562	15	0.9	825	4	US-09-543-681A-2474	Sequence 2474, App	635	15	0.9	1018	3	US-08-460-736-194	Sequence 194, App
563	15	0.9	831	3	US-09-342-681C-10	Sequence 10, Appl	636	15	0.9	1018	3	US-09-535-770-194	Sequence 194, App
564	15	0.9	845	1	US-08-378-011A-2	Sequence 2, Appl1	637	15	0.9	1018	4	US-09-653-667-194	Sequence 194, App
565	15	0.9	846	4	US-09-247-890-9	Sequence 9, Appl1	638	15	0.9	1019	3	US-09-056-105-13	Sequence 13, Appl
566	15	0.9	846	4	US-09-724-969-9	Sequence 9, Appl1	639	15	0.9	1019	3	US-09-270-767-9786	Sequence 9786, App
567	15	0.9	846	4	US-09-724-852-9	Sequence 9, Appl1	640	15	0.9	1019	4	US-09-270-767-25068	Sequence 25068, App
568	15	0.9	846	6	5164485-1	Patent No. 5164485	641	15	0.9	1019	4	US-09-270-767-25068	Sequence 25068, App
569	15	0.9	859	4	US-09-328-352-2632	Sequence 2632, App	642	15	0.9	1020	4	US-09-107-532A-3233	Sequence 3233, App
570	15	0.9	855	3	US-09-247-373B-37	Sequence 37, Appl	643	15	0.9	1022	3	US-09-222-575-67	Sequence 67, Appl
571	15	0.9	855	4	US-09-270-767-11359	Sequence 11359, App	644	15	0.9	1022	4	US-09-389-681-67	Sequence 67, Appl
572	15	0.9	871	5	PCT-US91-06234A-7	Sequence 7, Appl1	645	15	0.9	1022	4	US-09-620-405B-67	Sequence 67, Appl
573	15	0.9	876	3	US-09-167-513-1	Sequence 1, Appl1	646	15	0.9	1022	4	US-09-339-338-67	Sequence 67, Appl
574	15	0.9	885	4	US-09-252-991A-7716	Sequence 7716, App	647	15	0.9	1022	4	US-09-433-826B-67	Sequence 67, Appl
575	15	0.9	885	4	US-09-328-352-3427	Sequence 3427, App	648	15	0.9	1022	4	US-09-604-287A-67	Sequence 67, Appl
576	15	0.9	893	2	US-08-500-914A-1	Sequence 1, Appl1	649	15	0.9	1022	4	US-09-285-480-67	Sequence 67, Appl
577	15	0.9	900	1	US-07-990-965-4	Sequence 4, Appl1	650	15	0.9	1022	4	US-09-834-759-67	Sequence 67, Appl
578	15	0.9	900	4	US-09-583-110-330	Sequence 330, App	651	15	0.9	1022	4	US-09-590-751A-67	Sequence 67, Appl
579	15	0.9	900	4	US-09-861-451A-41	Sequence 41, Appl	652	15	0.9	1024	4	US-09-328-475C-65	Sequence 65, Appl
580	15	0.9	909	4	US-09-252-991A-5120	Sequence 5120, App	653	15	0.9	1026	4	US-09-489-039A-5619	Sequence 5619, App
581	15	0.9	909	4	US-09-328-352-1880	Sequence 1880, App	654	15	0.9	1037	3	US-08-858-207A-149	Sequence 149, App
582	15	0.9	912	4	US-09-248-796A-2401	Sequence 2401, App	655	15	0.9	1040	4	US-09-023-655-1487	Sequence 1487, App
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584	15	0.9	918	4	US-09-107-532A-2868	Sequence 2868, App	657	15	0.9	1062	4	US-09-248-796A-10507	Sequence 10507, App
585	15	0.9	918	4	US-09-107-532A-2870	Sequence 2870, App	658	15	0.9	1068	4	US-09-170-496D-1	Sequence 1, Appl1
586	15	0.9	918	4	US-09-107-532A-2871	Sequence 2871, App	659	15	0.9	1068	4	US-09-170-496D-163	Sequence 163, App
587	15	0.9	918	4	US-09-107-532A-2873	Sequence 2873, App	660	15	0.9	1068	4	US-09-328-352-996	Sequence 996, App
588	15	0.9	918	4	US-09-107-532A-2875	Sequence 2875, App	661	15	0.9	1095	4	US-09-248-796A-11826	Sequence 11826, App
589	15	0.9	918	4	US-09-107-532A-2877	Sequence 2877, App	662	15	0.9	1098	4	US-09-583-110-437	Sequence 437, App
590	15	0.9	921	4	US-09-011-143-6	Sequence 6, Appl1	663	15	0.9	1116	3	US-08-928-941D-17	Sequence 17, Appl
591	15	0.9	921	4	US-09-011-143-7	Sequence 7, Appl1	664	15	0.9	1116	3	US-09-280-580A-17	Sequence 17, Appl
592	15	0.9	921	4	US-09-302-495-6	Sequence 6, Appl1	665	15	0.9	1116	3	US-09-892-358-17	Sequence 17, Appl
593	15	0.9	921	4	US-09-302-495-7	Sequence 7, Appl1	666	15	0.9	1128	4	US-09-205-258-182	Sequence 182, App
594	15	0.9	921	4	US-10-079-616-6	Sequence 6, Appl1	667	15	0.9	1134	4	US-09-248-796A-6128	Sequence 6128, App
595	15	0.9	921	4	US-10-079-616-7	Sequence 7, Appl1	668	15	0.9	1149	4	US-09-970-516-5	Sequence 5, Appl1
596	15	0.9	932	4	US-09-526-597D-1	Sequence 1, Appl1	669	15	0.9	1149	4	US-09-970-516-5	Sequence 5, Appl1
597	15	0.9	933	4	US-09-526-597D-1	Sequence 1, Appl1	670	15	0.9	1164	4	US-09-489-039A-1222	Sequence 1222, App
598	15	0.9	933	4	US-09-107-532A-78	Sequence 78, Appl1	671	15	0.9	1167	4	US-09-583-110-704	Sequence 704, App
599	15	0.9	936	4	US-09-107-532A-531	Sequence 531, App	672	15	0.9	1178	4	US-09-270-767-26116	Sequence 26116, App
600	15	0.9	943	1	US-09-107-532A-1111	Sequence 1111, App	673	15	0.9	1182	4	US-09-252-991A-13631	Sequence 13631, App
601	15	0.9	943	1	US-07-807-043B-12	Sequence 12, Appl	674	15	0.9	1183	4	US-09-799-451-103	Sequence 203, App
602	15	0.9	943	2	US-08-299-849B-12	Sequence 12, Appl	675	15	0.9	1185	1	US-07-757-536B-5	Sequence 5, Appl1
603	15	0.9	943	2	US-08-142-368A-12	Sequence 12, Appl	676	15	0.9	1188	4	US-07-757-536B-4	Sequence 4, Appl1
604	15	0.9	943	3	US-08-967-727-12	Sequence 12, Appl	677	15	0.9	1188	4	US-07-757-536B-4	Sequence 4, Appl1
605	15	0.9	943	3	US-08-037-230D-12	Sequence 12, Appl	678	15	0.9	1200	3	US-08-854-531-5	Sequence 5, Appl1
606	15	0.9	943	4	US-09-583-850-12	Sequence 12, Appl	679	15	0.9	1200	5	US-09-107-532A-1060	Sequence 1060, App
607	15	0.9	943	4	US-09-579-197-12	Sequence 12, Appl	680	15	0.9	1200	5	PCT-US95-13552-5	Sequence 5, Appl1
608	15	0.9	943	4	US-09-404-026-12	Sequence 12, Appl	681	15	0.9	1203	4	US-09-134-000C-2824	Sequence 2824, App
609	15	0.9	945	3	US-09-312-464-12	Sequence 12, Appl	682	15	0.9	1203	4	US-09-461-325-14	Sequence 14, Appl
610	15	0.9	945	3	US-09-056-105-7	Sequence 7, Appl1	683	15	0.9	1208	4	US-10-012-542-14	Sequence 14, Appl
611	15	0.9	948	3	US-09-392-714-19	Sequence 19, Appl	684	15	0.9	1208	4	US-10-115-123-14	Sequence 14, Appl
					US-09-247-155-50	Sequence 50, Appl							

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691	15	0.9	1260	4	US-09-583-110-2466	Sequence 2466, Ap
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C 694	15	0.9	1272	2	US-08-972-258-1	Sequence 1, Appli
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696	15	0.9	1272	4	US-09-641-111A-1	Sequence 968, App
697	15	0.9	1277	4	US-09-620-312D-968	Sequence 1380, Ap
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C 699	15	0.9	1283	4	US-09-976-594-58	Sequence 1332, Ap
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713	15	0.9	1313	3	US-08-954-698-4	Sequence 4, Appli
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743	15	0.9	1365	3	US-09-221-245-6	Sequence 6, Appli
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C 766	15	0.9	1431	4	US-09-799-451-720	Sequence 720, App
C 767	15	0.9	1431	4	US-09-961-527-127	Sequence 327, App
C 768	15	0.9	1436	4	US-09-016-434-1426	Sequence 1426, Ap
769	15	0.9	1440	4	US-09-270-767-1608	Sequence 1608, Ap
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C 776	15	0.9	1451	3	US-08-826-025-14	Sequence 14, Appli
C 777	15	0.9	1451	3	US-09-826-025-14	Sequence 9, Appli
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C 779	15	0.9	1452	3	US-10-042-991-9	Sequence 5148, Ap
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C 781	15	0.9	1464	4	US-09-248-796A-5148	Sequence 27, Appli
C 782	15	0.9	1464	3	US-10-042-991-27	Sequence 10, Appli
C 783	15	0.9	1467	4	US-10-042-991-10	Sequence 2092, Ap
C 784	15	0.9	1479	4	US-09-543-681A-2092	Sequence 4920, Ap
C 785	15	0.9	1500	4	US-09-252-991A-4920	Sequence 23, App
C 786	15	0.9	1500	4	US-09-774-528-231	Sequence 643, App
787	15	0.9	1501	4	US-09-583-110-643	Sequence 1481, Ap
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789	15	0.9	1512	4	US-09-328-352-165	Sequence 10, Appli
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C 791	15	0.9	1535	1	US-09-499-227-10	Sequence 546, App
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C 793	15	0.9	1550	3	US-09-248-796A-549	Sequence 66, Appli
C 794	15	0.9	1551	4	US-09-461-325-66	Sequence 66, Appli
C 795	15	0.9	1558	4	US-10-012-542-66	Sequence 66, Appli
C 796	15	0.9	1558	4	US-10-115-123-66	Sequence 11, Appli
C 797	15	0.9	1558	4	US-08-751-767A-11	Sequence 1, Appli
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803	15	0.9	1576	3	US-09-058-376-2	Sequence 9, Appli
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C 806	15	0.9	1587	4	US-09-685-286-11	Sequence 11, Appli
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C 812	15	0.9	1640	2	US-08-299-849B-11	Sequence 11, Appli
C 813	15	0.9	1640	2	US-08-142-368A-11	Sequence 11, Appli
C 814	15	0.9	1640	3	US-08-967-727-11	Sequence 11, Appli
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C 816	15	0.9	1640	4	US-09-583-850-11	Sequence 11, Appli
C 817	15	0.9	1640	4	US-09-579-197-11	Sequence 11, Appli
C 818	15	0.9	1640	4	US-09-404-026-11	Sequence 11, Appli
C 819	15	0.9	1640	4	US-09-312-464-11	Sequence 11, Appli
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C 823	15	0.9	1653	4	US-09-248-796A-336	Sequence 336, App
C 824	15	0.9	1659	4	US-09-614-221A-234	Sequence 234, App
C 825	15	0.9	1665	4	US-09-221-017B-1017	Sequence 1017, App
C 826	15	0.9	1668	4	US-09-614-221A-420	Sequence 420, App
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C 830	15	0.9	1705	4	US-09-964-994B-6	Sequence 6, Appli

831	15	0.9	1713	4	US-09-489-039A-4371	Sequence 4371, Ap	C 904	15	0.9	2274	4	US-09-799-451-149	Sequence 149, App
832	15	0.9	1715	3	US-08-757-230A-1	Sequence 1, Appli	905	15	0.9	2291	2	US-08-725-736D-1	Sequence 1, Appli
833	15	0.9	1715	4	US-08-700-393-1	Sequence 1, Appli	906	15	0.9	2291	2	US-09-162-368B-1	Sequence 1, Appli
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C 836	15	0.9	1719	4	US-09-328-352-50	Sequence 50, Appli	C 909	15	0.9	2305	2	US-08-142-368A-17	Sequence 17, Appl
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C 839	15	0.9	1774	4	US-09-311-021-99	Sequence 99, Appl	C 912	15	0.9	2305	4	US-09-583-850-17	Sequence 17, Appl
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C 843	15	0.9	1854	4	US-09-543-681A-200	Sequence 200, App	916	15	0.9	2318	4	US-09-851-062-3	Sequence 3, Appli
844	15	0.9	1870	4	US-09-310-842-4	Sequence 4, Appli	917	15	0.9	2346	4	US-09-193-503B-4	Sequence 4, Appli
845	15	0.9	1875	2	US-08-683-743-3	Sequence 3, Appli	918	15	0.9	2346	3	US-09-193-503B-8	Sequence 8, Appli
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C 847	15	0.9	1926	4	US-09-248-796A-5825	Sequence 5825, Ap	920	15	0.9	2346	4	US-09-415-839-4	Sequence 4, Appli
C 848	15	0.9	1929	4	US-09-543-681A-3758	Sequence 3758, Ap	921	15	0.9	2346	4	US-09-415-839-5	Sequence 5, Appli
C 849	15	0.9	1929	4	US-09-248-796A-1277	Sequence 1277, Ap	922	15	0.9	2346	4	US-09-415-839-8	Sequence 8, Appli
850	15	0.9	1963	4	US-09-270-767-11063	Sequence 11063, A	923	15	0.9	2362	1	US-08-265-087-1	Sequence 1, Appli
851	15	0.9	1982	1	US-08-480-547A-12	Sequence 12, Appli	924	15	0.9	2362	1	US-08-621-493-1	Sequence 1, Appli
852	15	0.9	1982	1	US-08-250-847B-12	Sequence 12, Appli	925	15	0.9	2362	2	US-08-965-688-1	Sequence 1, Appli
853	15	0.9	1982	2	US-08-463-949A-12	Sequence 12, Appli	926	15	0.9	2362	3	US-09-260-173-1	Sequence 1, Appli
854	15	0.9	1982	3	US-08-464-410A-12	Sequence 12, Appli	927	15	0.9	2362	4	US-09-924-703-3	Sequence 3, Appli
855	15	0.9	1982	5	PCT-US94-06066-12	Sequence 12, Appli	928	15	0.9	2395	3	US-08-985-335-6	Sequence 6, Appli
856	15	0.9	1992	3	US-08-776-265-6	Sequence 6, Appli	929	15	0.9	2395	3	US-09-410-372-6	Sequence 6, Appli
857	15	0.9	1992	4	US-09-398-184-6	Sequence 6, Appli	930	15	0.9	2422	3	US-08-952-365-7	Sequence 7, Appli
858	15	0.9	2006	4	US-09-354-123-5	Sequence 5, Appli	C 931	15	0.9	2442	4	US-09-131-237C-1	Sequence 1, Appli
859	15	0.9	2009	4	US-09-809-665A-104	Sequence 104, App	C 932	15	0.9	2482	4	US-08-870-521-6	Sequence 6, Appli
860	15	0.9	2024	2	US-08-458-970A-1	Sequence 1, Appli	933	15	0.9	2524	4	US-08-961-527-742	Sequence 742, App
861	15	0.9	2031	4	US-09-252-991A-5180	Sequence 5180, Ap	C 934	15	0.9	2571	4	US-09-598-401C-93	Sequence 93, Appli
C 862	15	0.9	2034	4	US-09-252-991A-1531	Sequence 1531, Ap	935	15	0.9	2597	4	US-09-835-654-1	Sequence 1, Appli
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864	15	0.9	2059	4	US-09-604-978-5	Sequence 5, Appli	937	15	0.9	2645	1	US-08-250-847B-22	Sequence 22, Appli
865	15	0.9	2059	4	US-09-604-728-5	Sequence 5, Appli	938	15	0.9	2645	2	US-08-463-949A-22	Sequence 22, Appli
866	15	0.9	2059	4	US-10-325-878-5	Sequence 5, Appli	939	15	0.9	2645	5	US-08-464-410A-22	Sequence 22, Appli
867	15	0.9	2060	1	US-08-480-547A-11	Sequence 11, Appli	940	15	0.9	2645	5	PCT-US94-06066-22	Sequence 22, Appli
868	15	0.9	2060	1	US-08-250-847B-11	Sequence 11, Appli	941	15	0.9	2688	1	US-08-088-633-3	Sequence 3, Appli
869	15	0.9	2060	2	US-08-463-949A-11	Sequence 11, Appli	942	15	0.9	2688	1	US-08-245-756-3	Sequence 3, Appli
870	15	0.9	2060	3	US-08-464-410A-11	Sequence 11, Appli	943	15	0.9	2688	2	US-08-441-750-3	Sequence 3, Appli
871	15	0.9	2060	5	PCT-US94-06066-11	Sequence 11, Appli	944	15	0.9	2688	2	US-08-441-751-3	Sequence 3, Appli
C 872	15	0.9	2081	4	US-09-799-451-184	Sequence 184, App	945	15	0.9	2688	5	PCT-US92-02521-3	Sequence 3, Appli
C 873	15	0.9	2105	4	US-09-446-821A-1	Sequence 1, Appli	946	15	0.9	2709	4	US-09-107-532A-183	Sequence 183, App
874	15	0.9	2119	4	US-09-399-588-1	Sequence 1, Appli	947	15	0.9	2733	4	US-09-614-221A-372	Sequence 372, App
875	15	0.9	2120	3	US-09-221-235-4	Sequence 4, Appli	948	15	0.9	2734	4	US-09-620-312D-533	Sequence 533, App
876	15	0.9	2120	3	US-09-221-928-4	Sequence 4, Appli	949	15	0.9	2754	3	US-09-429-322D-3	Sequence 3, Appli
877	15	0.9	2120	3	US-09-221-527-4	Sequence 4, Appli	950	15	0.9	2802	4	US-09-976-534-924	Sequence 924, App
878	15	0.9	2120	3	US-09-221-236-4	Sequence 4, Appli	C 951	15	0.9	2896	2	US-08-709-923-1	Sequence 1, Appli
879	15	0.9	2120	3	US-09-221-416-4	Sequence 4, Appli	952	15	0.9	2903	3	US-08-928-941D-2	Sequence 2, Appli
880	15	0.9	2120	3	US-09-221-245-4	Sequence 4, Appli	953	15	0.9	2903	3	US-08-928-941D-3	Sequence 3, Appli
881	15	0.9	2120	3	US-09-163-115-4	Sequence 4, Appli	954	15	0.9	2903	3	US-08-280-590A-2	Sequence 2, Appli
882	15	0.9	2120	3	US-09-221-528-4	Sequence 4, Appli	955	15	0.9	2903	3	US-08-280-590A-3	Sequence 3, Appli
883	15	0.9	2120	3	US-09-593-553-4	Sequence 4, Appli	956	15	0.9	2903	4	US-09-892-398-2	Sequence 2, Appli
884	15	0.9	2120	3	US-09-221-237-4	Sequence 4, Appli	957	15	0.9	2903	4	US-09-892-398-3	Sequence 3, Appli
885	15	0.9	2120	4	US-09-757-982-4	Sequence 4, Appli	958	15	0.9	2909	3	US-08-104-158-1	Sequence 1, Appli
886	15	0.9	2122	4	US-09-710-279-4457	Sequence 4457, Ap	959	15	0.9	2909	4	US-09-609-040-1	Sequence 1, Appli
887	15	0.9	2166	4	US-09-134-000C-2061	Sequence 2061, Ap	960	15	0.9	2979	4	US-09-609-040-1	Sequence 1, Appli
888	15	0.9	2166	4	US-09-854-133-728	Sequence 728, App	961	15	0.9	2992	1	US-07-718-575-1	Sequence 1, Appli
889	15	0.9	2180	3	US-09-269-731-5	Sequence 5, Appli	962	15	0.9	2992	1	US-08-481-206-1	Sequence 1, Appli
C 890	15	0.9	2181	4	US-09-583-110-121	Sequence 121, App	963	15	0.9	2992	2	US-08-486-269A-1	Sequence 1, Appli
891	15	0.9	2193	4	US-09-011-143-5	Sequence 5, Appli	C 964	15	0.9	2998	4	US-09-710-279-3894	Sequence 3894, App
892	15	0.9	2193	4	US-09-302-495-5	Sequence 5, Appli	C 965	15	0.9	3006	4	US-09-248-796A-3676	Sequence 3676, App
893	15	0.9	2193	4	US-10-079-616-5	Sequence 5, Appli	C 966	15	0.9	3055	4	US-08-956-171E-297	Sequence 297, App
C 894	15	0.9	2226	1	US-08-299-849B-16	Sequence 16, Appli	C 967	15	0.9	3055	4	US-08-781-986A-297	Sequence 297, App
C 895	15	0.9	2226	2	US-08-142-368A-16	Sequence 16, Appli	C 968	15	0.9	3075	4	US-09-023-655-1369	Sequence 1369, App
C 896	15	0.9	2226	2	US-08-967-727-16	Sequence 16, Appli	C 969	15	0.9	3079	4	US-09-053-374A-6	Sequence 6, Appli
C 897	15	0.9	2226	3	US-08-037-230D-16	Sequence 16, Appli	C 970	15	0.9	3083	4	US-09-155-246-1	Sequence 1, Appli
C 898	15	0.9	2226	4	US-09-583-850-16	Sequence 16, Appli	971	15	0.9	3118	4	US-09-710-279-1798	Sequence 1798, App
C 899	15	0.9	2226	4	US-09-579-197-16	Sequence 16, Appli	972	15	0.9	3128	3	US-08-716-449-1	Sequence 1, Appli
C 900	15	0.9	2226	4	US-09-404-026-16	Sequence 16, Appli	C 973	15	0.9	3141	4	US-08-252-991A-13713	Sequence 13713, A
C 901	15	0.9	2226	4	US-09-312-464-16	Sequence 16, Appli	C 974	15	0.9	3150	3	US-08-673-814-5	Sequence 5, Appli
C 902	15	0.9	2230	4	US-09-620-312D-282	Sequence 282, App	C 975	15	0.9	3150	3	US-09-115-824-5	Sequence 5, Appli
C 903	15	0.9	2270	2	US-08-852-807-16	Sequence 16, Appli	976	15	0.9	3158	4	US-09-710-279-4054	Sequence 4054, App

978 15 0.9 3177 4 US-09-248-796A-5784 Sequence 5784, App
C 978 15 0.9 3182 4 US-09-155-885A-305 Sequence 305, App
C 979 15 0.9 3188 4 US-09-710-279-3837 Sequence 3837, App
C 980 15 0.9 3188 4 US-09-155-885A-293 Sequence 293, App
C 981 15 0.9 3200 4 US-09-155-885A-280 Sequence 280, App
982 15 0.9 3211 2 US-08-574-959A-8 Sequence 8, Appli
983 15 0.9 3211 3 US-09-357-014-8 Sequence 1, Appli
984 15 0.9 3212 3 US-08-673-814-1 Sequence 1, Appli
C 985 15 0.9 3212 3 US-09-115-824-1 Sequence 1, Appli
C 986 15 0.9 3212 4 US-09-155-885A-298 Sequence 298, App
C 987 15 0.9 3213 4 US-09-155-885A-288 Sequence 288, App
C 988 15 0.9 3213 4 US-09-155-885A-289 Sequence 289, App
C 989 15 0.9 3214 4 US-09-155-885A-294 Sequence 294, App
C 990 15 0.9 3215 4 US-09-719-528A-1 Sequence 1, Appli
C 991 15 0.9 3215 4 US-09-155-885A-290 Sequence 290, App
C 992 15 0.9 3215 4 US-09-155-885A-291 Sequence 291, App
C 993 15 0.9 3215 4 US-09-155-885A-292 Sequence 292, App
C 994 15 0.9 3215 4 US-09-155-885A-295 Sequence 295, App
C 995 15 0.9 3215 4 US-09-155-885A-296 Sequence 296, App
C 996 15 0.9 3215 4 US-09-155-885A-297 Sequence 297, App
C 997 15 0.9 3215 4 US-10-209-264-1 Sequence 1, Appli
C 998 15 0.9 3220 2 US-08-225-488-1 Sequence 1, Appli
C 999 15 0.9 3220 6 5196194-11 Patent No. 5196194
C1000 15 0.9 3220 6 5196194-15 Patent No. 5196194

ALIGNMENTS

RESULT 1
US-09-248-796A-11388
Sequence 11388, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 11388
LENGTH: 198
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-11388

Query Match 1.2%; Score 19; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1617 GGAGCTTGATTAAGTGCG 1635
Db 2 GGAGCTTGATTAAGTGCG 20

RESULT 2
US-08-956-171E-107
Sequence 107, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 2488 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-08-956-171E-107

Query Match 1.2%; Score 19; DB 4; Length 2488;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 923 AATATCAATCAAAATATTC 941
Db 1354 AATATCAATCAAAATATTC 1372

RESULT 3
US-08-781-986A-107
Sequence 107, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

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/ ATTORNEY/AGENT INFORMATION:
/ NAME: Benson, Bob
/ REGISTRATION NUMBER: 30,446
/ REFERENCE/DOCKET NUMBER: PB248BP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 107:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2488 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/
US-08-781-986A-107

Query Match 1.2%; Score 19; DB 4; Length 2488;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 923 AATATCAATCAAAATATTC 941
Db 1354 AATATCAATCAAAATATTC 1372

RESULT 4
US-09-513-999C-16375
/ Sequence 16375, Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclet, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ PATENT NO. 6783961
/ FILE REFERENCE: 59, US2, REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ CURRENT FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36661
/ SOFTWARE: Patent.pm
/ SEQ ID NO 16375
/ LENGTH: 125
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/
US-09-513-999C-16375

Query Match 1.1%; Score 18; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1111 GATAGCAAGAGAGTGTTA 1128
Db 49 GATAGCAAGAGAGTGTTA 66

RESULT 5
US-09-513-999C-23083
/ Sequence 23083, Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclet, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ PATENT NO. 6783961
/ FILE REFERENCE: 59, US2, REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ CURRENT FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36661
/ SOFTWARE: Patent.pm

/ SEQ ID NO 23083
/ LENGTH: 153
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/
US-09-513-999C-23083

Query Match 1.1%; Score 18; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1161 TGTTTTAATCCTCTGAC 1178
Db 107 TGTTTTAATCCTCTGAC 124

RESULT 6
US-09-134-001C-396/C
/ Sequence 396, Application US/09134001C
/ Patent No. 6380370
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/ TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: GTC-007
/ CURRENT APPLICATION NUMBER: US/09/134,001C
/ CURRENT FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/064,964
/ PRIOR FILING DATE: 1997-11-08
/ PRIOR APPLICATION NUMBER: US 60/055,779
/ PRIOR FILING DATE: 1997-08-14
/ NUMBER OF SEQ ID NOS: 5674
/ SEQ ID NO 396
/ LENGTH: 166
/ TYPE: DNA
/ ORGANISM: Staphylococcus epidermidis
/
US-09-134-001C-396

Query Match 1.1%; Score 18; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 954 AATATTTATTAACTTGA 971
Db 37 AATATTTATTAACTTGA 20

RESULT 7
US-09-389-681-371
/ Sequence 371, Application US/09389681A
/ Patent No. 6518237
/ GENERAL INFORMATION:
/ APPLICANT: Yuqi, Jiang
/ APPLICANT: Dillon, David C.
/ APPLICANT: Mitcham, Jennifer L.
/ APPLICANT: Xu, Jiangchun
/ TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
/ TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
/ FILE REFERENCE: 210121.470C3
/ CURRENT APPLICATION NUMBER: US/09/389,681A
/ CURRENT FILING DATE: 1999-09-02
/ NUMBER OF SEQ ID NOS: 463
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 371
/ LENGTH: 241
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1) - (1241)
/ OTHER INFORMATION: n = A,T,C or G
/
US-09-389-681-371

Query Match 1.1%; Score 18; DB 4; Length 241;
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 648 TTATTGAAGTGGCTTGA 665
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DB 98 TTATTGAAGTGGCTTGA 115

RESULT 8

US-09-620-405B-371
; Sequence 371, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 371
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-620-405B-371

Query Match 1.1%; Score 18; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 648 TTATTGAAGTGGCTTGA 665
|||
DB 98 TTATTGAAGTGGCTTGA 115

RESULT 9

US-09-433-826B-371
; Sequence 371, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 371
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-433-826B-371

Query Match 1.1%; Score 18; DB 4; Length 241;

Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 648 TTATTGAAGTGGCTTGA 665
|||
DB 98 TTATTGAAGTGGCTTGA 115

RESULT 10

US-09-604-287A-371
; Sequence 371, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
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; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-604-287A-371

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RESULT 11

US-09-834-759-371
; Sequence 371, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 371
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-759-371

Query Match 1.1%; Score 18; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 648 TTATTGAAGTGGCTTGA 665
|||||
Db 98 TTATTGAAGTGGCTTGA 115
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RESULT 12

US-09-590-751A-371
; Sequence 371, Application US/09590751A
; Patent No. 6756477

GENERAL INFORMATION:

APPLICANT: Yugui, Jiang
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jianshun
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C6
CURRENT APPLICATION NUMBER: US/09/590,751A
CURRENT FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 479
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 371
LENGTH: 241
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(241)
OTHER INFORMATION: n = A,T,C or G
US-09-590-751A-371

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 648 TTATTGAAGTGGCTTGA 665
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RESULT 13

US-09-643-597-325
; Sequence 325, Application US/09643597
; Patent No. 6426072

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hoeken, Nancy R.
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaeli A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 325
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapien

US-09-643-597-325

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Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14

US-09-480-884A-325
; Sequence 325, Application US/09480884A
; Patent No. 6482597

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Hoeken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 325
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapien
US-09-480-884A-325

Query Match 1.1%; Score 18; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1161 TGTTTTATCCTCTGAC 1178
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Db 269 TGTTTTATCCTCTGAC 286
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RESULT 15

US-09-542-615A-325
; Sequence 325, Application US/09542615A
; Patent No. 6518256

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hoeken, Nancy A.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 325
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapien
US-09-542-615A-325

Query Match 1.1%; Score 18; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1161 TGTTTTATCCTCTGAC 1178
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Db 269 TGTTTTAATCCTGAC 286

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OM nucleic - nucleic search, using bw model

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SUMMARIES

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6	19	1.2	453	16	US-10-276-774-400
7	19	1.2	656	16	US-10-424-599-8986
8	19	1.2	983	16	US-10-424-599-12542
9	19	1.2	1584	16	US-10-282-122A-9460
10	19	1.2	1719	17	US-10-437-963-76086
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C 173	17	1.0	525	13	US-10-027-632-317704	Sequence 317704, A
C 174	17	1.0	525	13	US-10-027-632-317705	Sequence 317705, A
C 175	17	1.0	525	15	US-10-027-632-91327	Sequence 91327, A
C 176	17	1.0	525	15	US-10-027-632-91328	Sequence 91328, A
C 177	17	1.0	525	15	US-10-027-632-91329	Sequence 91329, A
C 178	17	1.0	525	15	US-10-027-632-317703	Sequence 317703, A
C 179	17	1.0	525	15	US-10-027-632-317704	Sequence 317704, A
C 180	17	1.0	525	15	US-10-027-632-317705	Sequence 317705, A
C 181	17	1.0	527	13	US-10-027-632-278153	Sequence 278153, A
C 182	17	1.0	527	15	US-10-027-632-278153	Sequence 278153, A
C 183	17	1.0	528	16	US-10-424-599-134518	Sequence 134518, A
C 184	17	1.0	547	9	US-09-864-761-12626	Sequence 12626, A
C 185	17	1.0	549	14	US-10-198-846-11582	Sequence 11582, A
C 186	17	1.0	555	13	US-10-027-632-44367	Sequence 44367, A
C 187	17	1.0	555	15	US-10-027-632-44367	Sequence 44367, A
C 188	17	1.0	574	10	US-09-814-353-19715	Sequence 19715, A
C 189	17	1.0	576	9	US-09-988-598-2232	Sequence 2232, App
C 190	17	1.0	589	17	US-10-021-323-722	Sequence 722, App
C 191	17	1.0	590	13	US-10-027-632-67596	Sequence 67596, A
C 192	17	1.0	590	13	US-10-027-632-311412	Sequence 311412, A
C 193	17	1.0	590	15	US-10-027-632-67596	Sequence 67596, A
C 194	17	1.0	590	15	US-10-027-632-311412	Sequence 311412, A
C 195	17	1.0	590	16	US-10-424-599-14605	Sequence 14605, A
C 196	17	1.0	593	10	US-09-822-846-214	Sequence 214, App
C 197	17	1.0	603	13	US-10-027-632-44575	Sequence 44575, A
C 198	17	1.0	603	15	US-10-027-632-44575	Sequence 44575, A
C 199	17	1.0	612	16	US-10-424-599-47883	Sequence 47883, A
C 200	17	1.0	622	13	US-10-027-632-90780	Sequence 90780, A
C 201	17	1.0	622	13	US-10-027-632-90781	Sequence 90781, A
C 202	17	1.0	622	15	US-10-027-632-90780	Sequence 90780, A
C 203	17	1.0	622	15	US-10-027-632-90781	Sequence 90781, A
C 204	17	1.0	625	16	US-10-424-599-128229	Sequence 128229, A
C 205	17	1.0	628	13	US-10-027-632-243608	Sequence 243608, A
C 206	17	1.0	628	15	US-10-027-632-243608	Sequence 243608, A
C 207	17	1.0	643	17	US-10-767-701-5903	Sequence 5903, App
C 208	17	1.0	645	13	US-10-027-632-240102	Sequence 240102, A
C 209	17	1.0	645	15	US-10-027-632-240102	Sequence 240102, A
C 210	17	1.0	649	16	US-10-424-599-135113	Sequence 135113, A
C 211	17	1.0	656	13	US-10-027-632-66140	Sequence 66140, A
C 212	17	1.0	656	15	US-10-027-632-66140	Sequence 66140, A
C 213	17	1.0	663	9	US-09-841-132-409	Sequence 409, App
C 214	17	1.0	663	13	US-10-027-632-88922	Sequence 88922, A
C 215	17	1.0	663	13	US-10-027-632-320486	Sequence 320486, A
C 216	17	1.0	663	15	US-10-027-632-88922	Sequence 88922, A
C 217	17	1.0	663	15	US-10-027-632-320486	Sequence 320486, A
C 218	17	1.0	670	13	US-10-027-632-109990	Sequence 109990, A
C 219	17	1.0	670	13	US-10-027-632-109991	Sequence 109991, A
C 220	17	1.0	670	15	US-10-027-632-109990	Sequence 109990, A
C 221	17	1.0	670	15	US-10-027-632-109991	Sequence 109991, A
C 222	17	1.0	704	13	US-10-027-632-70647	Sequence 70647, A
C 223	17	1.0	704	15	US-10-027-632-70647	Sequence 70647, A
C 224	17	1.0	708	17	US-10-767-795-250	Sequence 250, App
C 225	17	1.0	723	18	US-10-425-115-158251	Sequence 158251, A
C 226	17	1.0	727	13	US-10-027-632-117525	Sequence 117525, A
C 227	17	1.0	727	15	US-10-027-632-117525	Sequence 117525, A
C 228	17	1.0	729	17	US-10-767-701-26740	Sequence 26740, A
C 229	17	1.0	736	13	US-10-027-632-147995	Sequence 147995, A
C 230	17	1.0	736	13	US-10-027-632-147996	Sequence 147996, A
C 231	17	1.0	736	15	US-10-027-632-147995	Sequence 147995, A

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C 234	17	1.0	742	15	US-10-027-632-72520	Sequence 27520, A	C 307	17	1.0	2026	18	US-10-425-115-174840	Sequence 174840, Ap
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C 236	17	1.0	753	13	US-10-027-632-167628	Sequence 167628,	C 309	17	1.0	2154	9	US-09-801-368-775	Sequence 375, Ap
C 237	17	1.0	753	13	US-10-027-632-167628	Sequence 167628,	C 310	17	1.0	2194	16	US-10-424-599-106594	Sequence 106594,
C 238	17	1.0	754	16	US-10-305-720-43	Sequence 43, Appl	C 311	17	1.0	2200	8	US-08-899-112-9	Sequence 9, Appl1
C 239	17	1.0	760	10	US-09-873-367C-963	Sequence 963, Appl	C 312	17	1.0	2200	15	US-10-398-992-3	Sequence 9, Appl1
C 240	17	1.0	760	11	US-09-968-007A-513	Sequence 513, Ap	C 313	17	1.0	2200	15	US-10-385-019-9	Sequence 9, Appl1
C 241	17	1.0	764	18	US-10-425-115-89839	Sequence 89839, A	C 314	17	1.0	2217	15	US-10-369-493-25507	Sequence 25507, A
C 242	17	1.0	784	16	US-10-424-599-106597	Sequence 106597,	C 315	17	1.0	2235	16	US-10-282-122A-41550	Sequence 41550, A
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C 244	17	1.0	793	10	US-09-925-302-349	Sequence 349, App	C 317	17	1.0	2310	16	US-10-282-122A-18020	Sequence 18020, A
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C 246	17	1.0	803	15	US-10-295-027-964	Sequence 964, App	C 319	17	1.0	2366	16	US-10-424-599-106595	Sequence 106595, A
C 247	17	1.0	803	16	US-10-058-270A-99	Sequence 99, Appl	C 320	17	1.0	2380	17	US-10-437-963-16586	Sequence 16586, A
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C 250	17	1.0	807	13	US-10-078-929-7	Sequence 7, Appl1	C 323	17	1.0	2520	15	US-10-094-749-122	Sequence 122, App
C 251	17	1.0	809	17	US-10-437-963-65162	Sequence 65162, A	C 324	17	1.0	2548	15	US-10-177-573-4	Sequence 4, Appl1
C 252	17	1.0	810	16	US-10-282-122A-7140	Sequence 7140, Ap	C 325	17	1.0	2553	17	US-10-437-963-11782	Sequence 11782, A
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C 255	17	1.0	834	15	US-10-369-493-34753	Sequence 34753, A	C 328	17	1.0	2732	17	US-10-377-139-17	Sequence 17, Appl
C 256	17	1.0	846	14	US-10-144-929-62	Sequence 62, Appl	C 329	17	1.0	2773	17	US-10-437-963-34050	Sequence 34050, A
C 257	17	1.0	846	16	US-10-144-929-62	Sequence 62, Appl	C 330	17	1.0	2781	16	US-10-108-260A-785	Sequence 785, App
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C 259	17	1.0	883	13	US-10-027-632-120498	Sequence 120498,	C 332	17	1.0	2799	14	US-10-125-540-220	Sequence 220, App
C 260	17	1.0	883	15	US-10-027-632-120497	Sequence 120497,	C 333	17	1.0	2822	16	US-10-102-260A-1263	Sequence 1263, Ap
C 261	17	1.0	883	15	US-10-027-632-120498	Sequence 120498,	C 334	17	1.0	2975	16	US-10-398-821-2005	Sequence 2005, Ap
C 262	17	1.0	926	16	US-10-260-238-5103	Sequence 5103, Ap	C 335	17	1.0	3044	9	US-09-764-870-98	Sequence 98, Appl
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C 265	17	1.0	1043	15	US-10-027-632-252199	Sequence 252199,	C 338	17	1.0	3140	15	US-10-369-493-26760	Sequence 26760, A
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C 267	17	1.0	1083	11	US-09-938-842A-2223	Sequence 2223, Ap	C 340	17	1.0	3146	18	US-10-425-115-3092	Sequence 3092, Ap
C 268	17	1.0	1098	13	US-10-027-632-308014	Sequence 308014,	C 341	17	1.0	3150	17	US-10-437-963-7292	Sequence 7292, Ap
C 269	17	1.0	1098	15	US-10-027-632-308014	Sequence 308014,	C 342	17	1.0	3433	16	US-10-424-599-128232	Sequence 128232,
C 270	17	1.0	1272	16	US-10-425-114-35730	Sequence 35730, A	C 343	17	1.0	3524	17	US-10-437-963-7632	Sequence 7632, Ap
C 271	17	1.0	1300	13	US-10-027-632-90782	Sequence 90782, A	C 344	17	1.0	3546	17	US-10-437-963-54272	Sequence 54272, A
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C 273	17	1.0	1311	18	US-10-425-115-181250	Sequence 181250,	C 346	17	1.0	3715	15	US-10-094-749-1066	Sequence 1066, Ap
C 274	17	1.0	1388	9	US-09-954-456-1149	Sequence 1149, Ap	C 347	17	1.0	3846	16	US-10-398-221-3646	Sequence 3646, Ap
C 275	17	1.0	1388	9	US-09-954-456-1814	Sequence 1814, Ap	C 348	17	1.0	4071	16	US-10-161-827-23	Sequence 23, Appl
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C 279	17	1.0	1462	17	US-10-437-963-31823	Sequence 31823, A	C 352	17	1.0	4226	15	US-10-117-722-480	Sequence 480, App
C 280	17	1.0	1500	16	US-10-424-599-15802	Sequence 15802, A	C 353	17	1.0	4226	15	US-10-117-722-480	Sequence 480, App
C 281	17	1.0	1521	16	US-10-424-599-59503	Sequence 59503, A	C 354	17	1.0	4277	18	US-10-425-115-26494	Sequence 26494, A
C 282	17	1.0	1551	15	US-10-369-493-5615	Sequence 4615, A	C 355	17	1.0	4674	16	US-10-321-625-202	Sequence 202, App
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C 287	17	1.0	1683	15	US-10-115-831-22	Sequence 22, Appl	C 360	17	1.0	6002	15	US-10-126-704-4	Sequence 4, Appl1
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C 296	17	1.0	1934	15	US-10-369-493-44979	Sequence 44979, A	C 369	17	1.0	25231	17	US-09-764-891-580	Sequence 580, Ap
C 297	17	1.0	1959	18	US-10-425-115-158511	Sequence 158511,	C 370	17	1.0	28001	15	US-10-173-817-11	Sequence 11, Appl
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C 407	17	1.0	174566	14	US-10-020-141-1	Sequence 37, App1	C 480	16	1.0	212	17	US-10-764-324-6002	Sequence 6002, App
C 408	17	1.0	197997	9	US-09-822-246-3	Sequence 3, App1	C 481	16	1.0	215	9	US-09-960-352-10302	Sequence 10302, App
C 409	17	1.0	208700	17	US-10-388-838-4	Sequence 4, App1	C 482	16	1.0	220	15	US-10-029-386-21335	Sequence 21335, A
C 410	17	1.0	220224	13	US-10-087-192-1282	Sequence 182, App	C 483	16	1.0	225	16	US-10-424-599-103228	Sequence 103228, A
C 411	17	1.0	275449	13	US-10-087-192-520	Sequence 520, App	C 484	16	1.0	233	9	US-09-232-758-141	Sequence 141, App
C 412	17	1.0	295096	13	US-10-087-192-331	Sequence 331, App	C 485	16	1.0	237	10	US-09-814-353-14029	Sequence 14029, A
C 413	17	1.0	317876	17	US-10-741-601-5629	Sequence 5629, App	C 486	16	1.0	239	9	US-09-983-965-5783	Sequence 5783, App
C 414	17	1.0	335913	10	US-09-754-853A-2	Sequence 2, App1	C 487	16	1.0	242	18	US-10-425-115-144399	Sequence 144399, A
C 415	17	1.0	335913	10	US-09-754-853A-3	Sequence 3, App1	C 488	16	1.0	245	16	US-10-422-535A-5776	Sequence 5776, App
C 416	17	1.0	374849	13	US-10-087-192-1627	Sequence 1627, App	C 489	16	1.0	245	16	US-10-085-783A-5776	Sequence 5776, App
C 417	17	1.0	397658	9	US-09-813-320-3	Sequence 3, App1	C 490	16	1.0	249	13	US-10-016-634-48	Sequence 48, App1
C 418	17	1.0	397658	9	US-09-813-320-3	Sequence 3, App1	C 491	16	1.0	249	17	US-10-437-963-8131	Sequence 8131, App
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C 420	17	1.0	518360	17	US-10-367-094-125	Sequence 125, App	C 493	16	1.0	250	10	US-09-814-353-7536	Sequence 7536, App
C 421	17	1.0	684187	17	US-10-367-094-71	Sequence 71, App1	C 494	16	1.0	260	14	US-10-010-731-13	Sequence 13, App1
C 422	17	1.0	1163020	16	US-10-398-821-10	Sequence 10, App1	C 495	16	1.0	252	13	US-10-071-751-46	Sequence 46, App1
C 423	17	1.0	1503841	9	US-09-795-668-1	Sequence 1, App1	C 496	16	1.0	255	10	US-09-814-353-13922	Sequence 13922, A
C 424	17	1.0	1503841	9	US-09-795-668-1	Sequence 1, App1	C 497	16	1.0	255	10	US-09-930-213-465	Sequence 465, App
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C 426	17	1.0	1691139	14	US-10-067-514-1	Sequence 1, App1	C 499	16	1.0	258	14	US-10-040-862-3471	Sequence 3471, App
C 427	17	1.0	1691139	16	US-10-419-723-1	Sequence 1, App1	C 500	16	1.0	258	16	US-10-057-4785-3471	Sequence 3471, App
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C 429	17	1.0	2140405	15	US-10-027-632-76212	Sequence 76212, A	C 502	16	1.0	258	17	US-10-764-324-3471	Sequence 3471, App
C 430	17	1.0	3011208	16	US-10-398-821-2058	Sequence 2058, App	C 503	16	1.0	259	9	US-09-294-093B-886	Sequence 886, App
C 431	17	1.0	3673778	15	US-10-312-841-1	Sequence 1, App1	C 504	16	1.0	261	9	US-09-983-965-5887	Sequence 5887, App
C 432	17	1.0	3673778	15	US-10-312-841-2	Sequence 2, App1	C 505	16	1.0	268	9	US-09-864-761-21966	Sequence 21966, A
C 433	16	1.0	25	10	US-09-771-933-27	Sequence 27, App1	C 506	16	1.0	269	16	US-10-424-599-94208	Sequence 94208, A
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C 435	16	1.0	25	10	US-09-771-933-35	Sequence 35, App1	C 508	16	1.0	271	9	US-09-894-924-5	Sequence 5, App1
C 436	16	1.0	25	10	US-09-771-933-205	Sequence 205, App	C 509	16	1.0	271	16	US-10-456-819-5	Sequence 5, App1
C 437	16	1.0	25	15	US-10-098-263B-64897	Sequence 64897, A	C 510	16	1.0	271	17	US-10-688-132-5	Sequence 5, App1
C 438	16	1.0	25	15	US-10-098-263B-111372	Sequence 111372, A	C 511	16	1.0	273	9	US-09-764-877-2492	Sequence 2492, App
C 439	16	1.0	60	10	US-09-908-975-5324	Sequence 5324, App	C 512	16	1.0	273	9	US-09-764-877-2493	Sequence 2493, App
C 440	16	1.0	65	10	US-09-908-975-1511	Sequence 1511, App	C 513	16	1.0	273	16	US-10-242-515-2452	Sequence 2452, App
C 441	16	1.0	88	15	US-10-029-386-14801	Sequence 14801, A	C 514	16	1.0	273	16	US-10-242-515-2453	Sequence 2453, App
C 442	16	1.0	112	10	US-09-764-891-10079	Sequence 10079, A	C 515	16	1.0	277	9	US-09-896-096A-7	Sequence 7, App1
C 443	16	1.0	112	10	US-09-764-891-10080	Sequence 10080, A	C 516	16	1.0	277	9	US-09-894-924-7	Sequence 7, App1
C 444	16	1.0	112	15	US-10-205-428-989	Sequence 989, App	C 517	16	1.0	277	16	US-10-456-819-7	Sequence 7, App1
C 445	16	1.0	112	15	US-10-205-428-990	Sequence 990, App	C 518	16	1.0	277	17	US-10-688-132-7	Sequence 7, App1
C 446	16	1.0	116	9	US-09-864-761-27222	Sequence 27222, A	C 519	16	1.0	278	10	US-09-814-353-13920	Sequence 13920, A
C 447	16	1.0	116	16	US-10-424-599-36191	Sequence 36191, A	C 520	16	1.0	283	9	US-09-896-096A-10	Sequence 10, App1
C 448	16	1.0	122	16	US-10-424-599-92078	Sequence 92078, A	C 521	16	1.0	283	9	US-09-894-924-10	Sequence 10, App1
C 449	16	1.0	125	17	US-10-437-963-96352	Sequence 96352, A	C 522	16	1.0	283	16	US-10-456-819-10	Sequence 10, App1
C 450	16	1.0	129	9	US-09-864-761-28284	Sequence 28284, A	C 523	16	1.0	283	17	US-10-688-132-10	Sequence 10, App1

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526	16	1.0	294	18	US-10-425-115-154141	Sequence 154141, Ap
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530	16	1.0	304	17	US-10-437-963-3627	Sequence 3627, Ap
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533	16	1.0	312	10	US-09-814-353-7525	Sequence 7526, Ap
534	16	1.0	314	16	US-10-424-599-80113	Sequence 80113, A
535	16	1.0	317	10	US-09-814-353-1210	Sequence 1210, Ap
536	16	1.0	317	10	US-09-814-353-7576	Sequence 7576, Ap
537	16	1.0	318	18	US-10-425-115-58457	Sequence 58457, A
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539	16	1.0	322	10	US-09-814-353-7558	Sequence 7558, Ap
540	16	1.0	324	10	US-09-814-353-1223	Sequence 1223, Ap
541	16	1.0	324	10	US-09-814-353-7588	Sequence 7588, Ap
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546	16	1.0	328	10	US-09-814-353-9569	Sequence 9569, Ap
547	16	1.0	334	17	US-10-437-963-2683	Sequence 2683, A
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552	16	1.0	344	10	US-09-814-353-7600	Sequence 7600, Ap
553	16	1.0	347	10	US-09-814-353-1256	Sequence 1256, Ap
554	16	1.0	347	10	US-09-814-353-7620	Sequence 7620, Ap
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556	16	1.0	348	16	US-10-085-783A-10328	Sequence 10328, A
557	16	1.0	350	10	US-09-814-353-1300	Sequence 1300, Ap
558	16	1.0	350	10	US-09-814-353-7664	Sequence 7664, Ap
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561	16	1.0	352	10	US-09-814-353-7571	Sequence 7571, Ap
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563	16	1.0	352	16	US-10-085-783A-11300	Sequence 11300, A
564	16	1.0	353	10	US-09-814-353-14005	Sequence 14005, A
565	16	1.0	353	14	US-10-062-727-1031	Sequence 1031, Ap
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573	16	1.0	357	9	US-09-764-877-2816	Sequence 2816, Ap
574	16	1.0	357	10	US-09-814-353-13984	Sequence 13984, A
575	16	1.0	357	16	US-10-242-515-2816	Sequence 2816, Ap
576	16	1.0	358	18	US-10-674-124A-9338	Sequence 9338, Ap
577	16	1.0	360	10	US-09-814-353-1243	Sequence 1243, Ap
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581	16	1.0	362	10	US-09-814-353-13950	Sequence 13950, A
582	16	1.0	363	10	US-09-814-353-1257	Sequence 1257, Ap
583	16	1.0	363	16	US-09-814-353-7621	Sequence 7621, Ap
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592	16	1.0	369	10	US-09-814-353-15953	Sequence 15953, A
593	16	1.0	370	10	US-09-814-353-1304	Sequence 1304, Ap
594	16	1.0	370	10	US-09-814-353-7668	Sequence 7668, Ap
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596	16	1.0	373	10	US-09-814-353-13973	Sequence 13973, A
597	16	1.0	375	9	US-09-777-564-152	Sequence 152, App
598	16	1.0	375	9	US-09-777-564-1498	Sequence 1488, Ap
599	16	1.0	375	14	US-10-015-219-152	Sequence 152, App
600	16	1.0	375	14	US-10-015-219-1488	Sequence 1488, Ap
601	16	1.0	378	10	US-09-814-353-1270	Sequence 1270, Ap
602	16	1.0	378	10	US-09-814-353-7634	Sequence 7634, Ap
603	16	1.0	381	9	US-09-815-242-1231	Sequence 1231, Ap
604	16	1.0	381	9	US-09-815-242-3315	Sequence 3315, Ap
605	16	1.0	381	16	US-10-282-122A-5809	Sequence 5809, Ap
606	16	1.0	381	16	US-10-282-122A-5887	Sequence 5887, Ap
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608	16	1.0	386	10	US-09-814-353-7566	Sequence 7566, Ap
609	16	1.0	387	10	US-09-814-353-1164	Sequence 1164, Ap
610	16	1.0	387	10	US-09-814-353-1299	Sequence 1299, Ap
611	16	1.0	387	10	US-09-814-353-7530	Sequence 7530, Ap
612	16	1.0	387	10	US-09-814-353-7663	Sequence 7663, Ap
613	16	1.0	390	9	US-09-960-352-5576	Sequence 6576, Ap
614	16	1.0	390	10	US-09-814-353-1244	Sequence 1244, Ap
615	16	1.0	390	10	US-09-814-353-7608	Sequence 7608, Ap
616	16	1.0	391	16	US-10-424-599-28865	Sequence 28865, A
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619	16	1.0	394	10	US-09-814-353-1251	Sequence 1251, Ap
620	16	1.0	394	10	US-09-814-353-7453	Sequence 7453, Ap
621	16	1.0	394	10	US-09-814-353-7615	Sequence 7615, Ap
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623	16	1.0	397	16	US-10-424-599-67060	Sequence 67060, A
624	16	1.0	399	10	US-09-918-995-7822	Sequence 7822, Ap
625	16	1.0	400	9	US-09-964-824A-19	Sequence 19, App1
626	16	1.0	400	10	US-09-814-353-13999	Sequence 13999, A
627	16	1.0	400	11	US-09-968-007A-41	Sequence 41, App1
628	16	1.0	400	10	US-09-814-353-1124	Sequence 1124, Ap
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634	16	1.0	404	10	US-09-814-353-1275	Sequence 1275, Ap
635	16	1.0	404	10	US-09-814-353-7639	Sequence 7639, Ap
636	16	1.0	404	10	US-09-814-353-13911	Sequence 13911, A
637	16	1.0	404	16	US-10-424-599-1622	Sequence 1622, Ap
638	16	1.0	405	10	US-09-814-353-1208	Sequence 1208, Ap
639	16	1.0	405	10	US-09-814-353-7574	Sequence 7574, Ap
640	16	1.0	406	10	US-09-814-353-1141	Sequence 1141, Ap
641	16	1.0	406	10	US-09-814-353-7507	Sequence 7507, Ap
642	16	1.0	407	9	US-09-960-352-931	Sequence 931, App
643	16	1.0	407	10	US-09-814-353-1233	Sequence 1233, Ap
644	16	1.0	407	10	US-09-814-353-1250	Sequence 1250, Ap
645	16	1.0	407	10	US-09-814-353-7598	Sequence 7598, Ap
646	16	1.0	409	10	US-09-814-353-7614	Sequence 7614, Ap
647	16	1.0	409	10	US-09-814-353-1142	Sequence 1142, Ap
648	16	1.0	409	10	US-09-814-353-1287	Sequence 1287, Ap
649	16	1.0	409	10	US-09-814-353-7508	Sequence 7508, Ap
650	16	1.0	409	10	US-09-814-353-7661	Sequence 7661, Ap
651	16	1.0	410	10	US-09-814-353-1215	Sequence 1215, Ap
652	16	1.0	410	10	US-09-814-353-7580	Sequence 7580, Ap
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654	16	1.0	411	16	US-10-424-599-81671	Sequence 81671, A
655	16	1.0	412	10	US-09-918-995-6491	Sequence 6491, Ap
656	16	1.0	413	10	US-09-814-353-1202	Sequence 1202, Ap
657	16	1.0	413	10	US-09-814-353-7568	Sequence 7568, Ap
658	16	1.0	413	18	US-10-425-115-79311	Sequence 79311, A
659	16	1.0	416	10	US-09-814-353-1232	Sequence 1222, Ap
660	16	1.0	416	10	US-09-814-353-1272	Sequence 1272, Ap
661	16	1.0	416	10	US-09-814-353-7567	Sequence 7567, Ap
662	16	1.0	416	10	US-09-814-353-7636	Sequence 7636, Ap
663	16	1.0	417	9	US-09-764-877-1478	Sequence 3787, Ap
664	16	1.0	417	16	US-10-131-827-8888	Sequence 8888, Ap
665	16	1.0	417	16	US-10-242-515-3478	Sequence 3478, Ap
666	16	1.0	417	18	US-10-425-115-65607	Sequence 65607, A
667	16	1.0	418	10	US-09-814-353-1279	Sequence 1279, Ap
668	16	1.0	418	10	US-09-814-353-1285	Sequence 1285, Ap
669	16	1.0	418	10	US-09-814-353-7643	Sequence 7643, Ap

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674	16	1.0	420	10	US-09-814-353-1151	Sequence 1151, Ap	747	16	1.0	454	10	US-09-814-353-1267	Sequence 1267, Ap
675	16	1.0	420	10	US-09-814-353-1253	Sequence 1253, Ap	748	16	1.0	454	10	US-09-814-353-7631	Sequence 7631, Ap
676	16	1.0	420	10	US-09-814-353-7517	Sequence 7517, Ap	749	16	1.0	454	10	US-09-814-353-13992	Sequence 13992, A
677	16	1.0	420	10	US-09-814-353-7617	Sequence 7617, Ap	750	16	1.0	454	10	US-09-814-353-14007	Sequence 14007, A
678	16	1.0	420	10	US-09-814-353-12701	Sequence 12701, A	751	16	1.0	455	10	US-09-814-353-1415	Sequence 1415, Ap
679	16	1.0	420	10	US-09-814-353-12700	Sequence 12700, A	752	16	1.0	455	10	US-09-814-353-7631	Sequence 7631, Ap
680	16	1.0	420	16	US-10-424-599-76325	Sequence 76325, A	753	16	1.0	457	10	US-09-814-353-14010	Sequence 14010, A
681	16	1.0	421	10	US-09-918-995-16853	Sequence 16853, A	754	16	1.0	458	9	US-09-864-761-10601	Sequence 10601, A
682	16	1.0	421	10	US-09-814-353-1213	Sequence 1213, Ap	755	16	1.0	458	9	US-09-864-761-13834	Sequence 13834, A
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684	16	1.0	421	10	US-09-814-353-13953	Sequence 13953, A	757	16	1.0	458	10	US-09-814-353-7555	Sequence 7555, Ap
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691	16	1.0	425	10	US-09-814-353-1229	Sequence 1229, Ap	764	16	1.0	460	16	US-10-356-736-32	Sequence 32, App1
692	16	1.0	425	10	US-09-814-353-7594	Sequence 7594, Ap	765	16	1.0	460	16	US-10-356-736-34	Sequence 34, App1
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694	16	1.0	427	10	US-09-814-353-13985	Sequence 13985, A	767	16	1.0	460	16	US-10-274-300-85	Sequence 85, App1
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c 980 16 1.0 529 9 US-09-814-353-15777 Sequence 15777, A
981 16 1.0 529 10 US-09-814-353-15777 Sequence 15777, A
c 982 16 1.0 529 11 US-09-969-034-3544 Sequence 3544, Ap
983 16 1.0 529 18 US-10-425-115-5511 Sequence 5511, Ap
c 984 16 1.0 531 9 US-09-884-441-5 Sequence 5, Appl1
985 16 1.0 531 9 US-09-974-300-6343 Sequence 6343, Ap
c 986 16 1.0 531 10 US-09-907-969-5 Sequence 5, Appl1
987 16 1.0 531 10 US-09-827-271-5 Sequence 5, Appl1
988 16 1.0 531 15 US-10-198-053-5 Sequence 5, Appl1
c 989 16 1.0 533 18 US-10-425-115-58724 Sequence 58724, A
990 16 1.0 533 10 US-09-814-353-1212 Sequence 1212, Ap
991 16 1.0 533 10 US-09-814-353-7578 Sequence 7578, Ap
992 16 1.0 536 10 US-09-814-353-13878 Sequence 13878, A
993 16 1.0 537 13 US-10-027-632-195778 Sequence 195778, A
994 16 1.0 537 13 US-10-027-632-195779 Sequence 195779, A
995 16 1.0 537 15 US-10-027-632-195778 Sequence 195778, A
996 16 1.0 537 15 US-10-027-632-195779 Sequence 195779, A
997 16 1.0 538 10 US-09-814-353-1234 Sequence 1234, Ap
998 16 1.0 538 10 US-09-814-353-7599 Sequence 7599, Ap
c 999 16 1.0 539 13 US-10-027-632-243606 Sequence 243606, A
c1000 16 1.0 539 15 US-10-027-632-243606 Sequence 243606, A
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ALIGNMENTS

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RESULT 1
US-10-425-114-3830
; Sequence 3830, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(533)3B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-26
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3830
; LENGTH: 1022
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700342511_FLI
US-10-425-114-3830
```

```
Query Match 1.2%; Score 20; DB 16; Length 1022;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 993 AGAACAAGCTTACTACACA 1012
|||||
Db 590 AGAACAAGCTTACTACACA 609
```

```
RESULT 2
US-10-425-115-67965
; Sequence 67965, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(533)22B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 67965
; LENGTH: 1718
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_161981C.1
US-10-425-115-67965
```

```
Query Match 1.2%; Score 20; DB 18; Length 1718;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 993 AGAACAAGCTTACTACACA 1012
|||||
Db 976 AGAACAAGCTTACTACACA 995
```

```
RESULT 3
US-09-764-891-9479/c
; Sequence 9479, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 9479
; LENGTH: 31140
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-9479
```

```
Query Match 1.2%; Score 20; DB 10; Length 31140;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 534 TGAACGCTTTAAACTCC 553
|||||
Db 25120 TGAACGCTTTAAACTCC 25101
```

```
RESULT 4
US-10-205-428-860/c
; Sequence 860, Application US/10205428
; Publication No. US20030108907A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA117C1
```

```
; CURRENT APPLICATION NUMBER: US/10/205,428
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 09/764,892
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1019
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 860
; LENGTH: 31140
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-428-860
```

```
Query Match      1.2%; Score 20; DB 15; Length 31140;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy      534 TGAACCTGCTTTAAACTCC 553
Db      25120 TGAACCTGCTTTAAACTCC 25101
```

```
RESULT 5
US-10-741-601-16635
; Sequence 16635, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO: 16635
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-16635
```

```
Query Match      1.2%; Score 19; DB 17; Length 201;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1206 TGTATTTTGCATATATGCT 1224
Db      179 TGTATTTTGCATATATGCT 197
```

```
RESULT 6
US-10-276-774-400/c
; Sequence 400, Application US/10276774
; Publication No. US2004005245A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO: 400
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-400
```

```
Query Match      1.2%; Score 19; DB 16; Length 453;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy      703 CTTCTTGCTTCTGTGAGG 721
Db      187 CTTCTTGCTTCTGTGAGG 169
```

```
RESULT 7
US-10-424-599-8986/c
; Sequence 8986, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO: 8986
; LENGTH: 656
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(656)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_108124C.1
US-10-424-599-8986
```

```
Query Match      1.2%; Score 19; DB 16; Length 656;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      635 TTGCACCAAAACATTATT 653
Db      266 TTGCACCAAAACATTATT 248
```

```
RESULT 8
US-10-424-599-125442
; Sequence 125442, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
```

```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 125442
; LENGTH: 983
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; LOCATION: (1)..(983)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_84284C.1
; US-10-424-599-125442

Query Match      1.2%; Score 19; DB 16; Length 983;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      526 TTGACCTTTGAACCTGCTT 544
      |||||
Db      89 TTGACCTTTGAACCTGCTT 107

RESULT 9
; US-10-282-122A-9460/C
; Sequence 9460, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haeselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9460
; LENGTH: 1584
; TYPE: DNA
```

```

; ORGANISM: Bacillus anthracis
; US-10-282-122A-9460

Query Match      1.2%; Score 19; DB 16; Length 1584;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      591 TAATATGCTTCGATAC 609
      |||||
Db      1564 TAATATGCTTCGATAC 1546

RESULT 10
; US-10-437-963-76086
; Sequence 76086, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 76086
; LENGTH: 1719
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_76111C.1
; US-10-437-963-76086

Query Match      1.2%; Score 19; DB 17; Length 1719;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      326 GGCTGACAGTGTCTTC 344
      |||||
Db      341 GGCTGACAGTGTCTTC 359

RESULT 11
; US-08-781-986A-107
; Sequence 107, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Shapylloccoccus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 2488 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-761-986A-107

Query Match 1.2%; Score 19; DB 8; Length 2488;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 923 AATATCAATCAAAATATTC 941
DB 1354 AATATCAATCAAAATATTC 1372

RESULT 12
US-10-329-624-107
Sequence 107, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gill H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/761,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 2488 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-10-329-624-107

Query Match 1.2%; Score 19; DB 16; Length 2488;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 923 AATATCAATCAAAATATTC 941
DB 1354 AATATCAATCAAAATATTC 1372

RESULT 13
US-10-424-599-117318
Sequence 117318, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 117318
LENGTH: 2625
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_76949C.1
US-10-424-599-117318

Query Match 1.2%; Score 19; DB 16; Length 2625;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 50 TTTTCTTCTGATTTGCGG 68
DB 432 TTTTCTTCTGATTTGCGG 450

RESULT 14
US-10-741-601-5741
Sequence 5741, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5741
LENGTH: 59247
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-601-5741

Query Match 1.2%; Score 19; DB 17; Length 59247;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 689 CTGTTGAGCTCCCTTCT 707
DB 10349 CTGTTGAGCTCCCTTCT 10367

RESULT 15
US-10-741-601-5641
; Sequence 5641, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5641
; LENGTH: 112486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(112486)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-601-5641

Query Match 1.2%; Score 19; DB 17; Length 112486;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 689 CTGTTGAGACTCTCTCTCT 707
DB 100878 CTGTTGAGACTCTCTCTCT 100896

Search completed: November 9, 2004, 10:30:35
Job time : 1341 secs